

Generic and Specific Adaptive Responses of *Streptococcus pneumoniae* to Challenge with Three Distinct Antimicrobial Peptides, Bacitracin, LL-37, and Nisin

Majchrzykiewicz, Joanna A.; Kuipers, Oscar P.; Bijlsma, Jetta J.E.

Published in:
Antimicrobial Agents and Chemotherapy

DOI:
[10.1128/AAC.00769-09](https://doi.org/10.1128/AAC.00769-09)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2010

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):
Majchrzykiewicz, J. A., Kuipers, O. P., & Bijlsma, J. J. E. (2010). Generic and Specific Adaptive Responses of *Streptococcus pneumoniae* to Challenge with Three Distinct Antimicrobial Peptides, Bacitracin, LL-37, and Nisin. *Antimicrobial Agents and Chemotherapy*, 54(1), 440-451. <https://doi.org/10.1128/AAC.00769-09>

Copyright
Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The information may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

Take-down policy
If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

SUPPLEMENTAL MATERIALS

Table S.1. Complete lists of differentially expressed genes of *S. pneumoniae* D39 exposure to bacitracin, nisin and LL-37 treatment.

Genes with a fold change of ≤ 0.6 or ≥ 1.5 are indicated in bold.

A. List of genes up-regulated upon **15 min.** treatment with **bacitracin:**

Gene ID	Ratio	Bayes.p	NCBI annotation
<i>SP0385</i>	2.1	2.40E-04	conserved hypothetical protein
<i>SP0386</i>	2.4	1.98E-05	putative sensor histidine kinase
<i>SP0387</i>	2.1	1.45E-04	DNA-binding response regulator
<i>SP0390</i>	2.1	1.77E-04	choline binding protein G
<i>SP0391</i>	2.0	2.76E-04	choline binding protein F
<i>SP0419</i>	1.8	5.79E-04	enoyl-(acyl-carrier-protein) reductase, <i>fabK</i>
<i>SP0420</i>	1.9	4.07E-04	CoA-acyl carrier protein transacylase, <i>fabD</i>
<i>SP0421</i>	2.0	1.25E-04	3-oxoacyl-[acyl-carrier protein] reductase, <i>fabG</i>
<i>SP0422</i>	2.2	6.31E-05	3-oxoacyl-(acyl-carrier-protein) synthase II, <i>fabF</i>
<i>SP0424</i>	2.2	4.39E-05	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase, <i>fabZ</i>
<i>SP0426</i>	2.1	2.19E-04	acetyl-CoA carboxylase, carboxyl transferase, beta subunit, <i>accD</i>
<i>SP0427</i>	2.4	1.54E-04	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit, <i>accA</i>
<i>SP0430</i>	2.3	7.12E-05	conserved domain protein
<i>SP0785</i>	1.8	1.92E-04	conserved hypothetical protein
<i>SP0786</i>	2.0	1.82E-04	ABC transporter, ATP-binding protein
<i>SP0787</i>	1.8	3.65E-04	conserved hypothetical protein
<i>SP0861</i>	1.7	4.39E-04	hypothetical protein
<i>SP0910</i>	1.6	4.96E-04	conserved hypothetical protein
<i>SP0912</i>	8.2	8.26E-11	ABC transporter, ATP-binding protein
<i>SP0913</i>	12.4	3.07E-10	putative ABC transporter, permease protein
<i>SP1356</i>	1.7	6.21E-04	amidohydrolase family protein
<i>SP1480</i>	1.4	7.87E-04	hypothetical protein
<i>SP1714</i>	2.9	5.93E-06	transcriptional regulator, GntR family
<i>SP1715</i>	2.3	1.20E-04	ABC transporter, ATP-binding protein

<i>SP1925</i>	1.8	6.85E-04	hypothetical protein
<i>SP1926</i>	1.8	7.32E-04	hypothetical protein
<i>SP2086</i>	1.9	9.20E-04	phosphate ABC transporter, permease protein, <i>pstA</i>

B. List of genes differentially expressed upon 30 min. treatment with bacitracin:

up-regulated genes				down-regulated genes			
Gene ID	Ratio	Bayes.p	NCBI annotation	Gene ID	Ratio	Bayes.p	NCBI annotation
<i>SP0069</i>	1.8	3.87E-05	choline binding protein I, <i>cbpI</i>	<i>SP0005</i>	0.5	4.41E-06	peptidyl-tRNA hydrolase
<i>SP0088</i>	2.1	2.94E-05	hypothetical protein	<i>SP0095</i>	0.2	2.68E-09	conserved hypothetical protein
<i>SP0101</i>	2.1	4.98E-06	putative transporter	<i>SP0117</i>	0.5	3.06E-05	pneumococcal surface protein A, <i>pspA</i>
<i>SP0107</i>	2.4	2.14E-06	LysM domain protein	<i>SP0281</i>	0.5	3.47E-05	aminopeptidase C
<i>SP0142</i>	2.0	2.39E-05	hypothetical protein	<i>SP0285</i>	0.5	2.88E-06	alcohol dehydrogenase, zinc-containing
<i>SP0157</i>	2.0	5.73E-05	hypothetical protein	<i>SP0366</i>	0.6	6.66E-05	oligopeptide ABC transporter, oligopeptide-binding protein AliA
<i>SP0189</i>	2.0	8.66E-06	conserved hypothetical protein	<i>SP0400</i>	0.5	1.45E-05	trigger factor
<i>SP0275</i>	2.3	5.13E-06	conserved hypothetical protein	<i>SP0430</i>	0.5	3.79E-06	conserved domain protein
<i>SP0276</i>	1.9	8.91E-05	conserved hypothetical protein	<i>SP0435</i>	0.5	3.93E-05	translation elongation factor P, <i>efp</i>
<i>SP0278</i>	2.1	3.62E-06	hypothetical protein	<i>SP0453</i>	0.6	9.90E-05	amino acid ABC transporter, amino acid-binding protein/permease protein
<i>SP0338</i>	3.1	8.59E-09	putative ATP-dependent Clp protease, ATP-binding subunit	<i>SP0458</i>	0.5	1.68E-05	DNA-damage inducible protein P
<i>SP0369</i>	1.9	1.53E-05	penicillin-binding protein 1A	<i>SP0459</i>	0.4	2.98E-08	formate acetyltransferase
<i>SP0370</i>	1.8	4.70E-05	recombination protein U	<i>SP0516</i>	0.6	2.46E-05	heat shock protein GrpE
<i>SP0371</i>	2.0	3.35E-05	conserved hypothetical protein	<i>SP0565</i>	0.4	6.87E-07	conserved domain protein
<i>SP0391</i>	1.7	9.72E-05	choline binding protein F	<i>SP0566</i>	0.4	1.02E-06	acetyltransferase, GNAT family

SP0408	2.6	2.29E-07	sodium:alanine symporter family protein	SP0568	0.5	1.87E-06	valyl-tRNA synthetase, <i>valS</i>
SP0487	1.9	9.29E-05	hypothetical protein	SP0577	0.4	1.33E-06	PTS system, beta-glucosides-specific IIABC components
SP0488	1.9	2.19E-06	conserved hypothetical protein	SP0579	0.5	2.73E-05	phenylalanyl-tRNA synthetase, alpha subunit, <i>pheS</i>
SP0582	2.5	2.41E-07	hypothetical protein	SP0580	0.6	5.64E-05	acetyltransferase, GNAT family
SP0607	2.3	4.15E-07	amino acid ABC transporter, permease protein	SP0581	0.5	1.43E-06	phenylalanyl-tRNA synthetase, beta subunit, <i>pheT</i>
SP0608	1.9	1.59E-05	amino acid ABC transporter, permease protein	SP0614	0.6	3.75E-05	tributylin esterase, <i>estA</i>
SP0609	1.9	1.34E-05	amino acid ABC transporter, amino acid-binding protein	SP0626	0.4	6.29E-07	branched-chain amino acid transport system II carrier protein <i>brnQ</i>
SP0641	3.0	1.26E-08	serine protease, subtilase family	SP0644	0.4	6.40E-06	hypothetical protein, truncation
SP0709	1.7	5.81E-05	amino acid ABC transporter, ATP-binding protein	SP0673	0.6	4.40E-05	hypothetical protein
SP0785	2.1	1.98E-06	conserved hypothetical protein	SP0731	0.5	1.48E-06	conserved domain protein
SP0786	2.3	3.40E-07	ABC transporter, ATP-binding protein	SP0736	0.6	7.06E-05	mannose-6-phosphate isomerase, <i>manA</i>
SP0787	2.4	5.55E-07	conserved hypothetical protein	SP0742	0.4	1.23E-07	conserved hypothetical protein
SP0790	2.3	2.89E-06	conserved domain protein	SP0745	0.6	8.51E-05	uracil phosphoribosyltransferase
SP0800	1.9	3.76E-05	hypothetical protein	SP0770	0.6	4.67E-05	ABC transporter, ATP-binding protein
SP0873	2.0	6.25E-06	membrane protein	SP0775	0.5	2.09E-06	ribosomal protein S16, <i>rpsP</i>
SP0875	2.1	2.56E-07	lactose phosphotransferase system repressor	SP0869	0.6	3.74E-05	aminotransferase, class-V
SP0876	2.2	2.30E-07	putative 1-phosphofructokinase	SP0870	0.5	5.24E-06	NifU family protein
SP0877	1.6	9.19E-05	PTS system, fructose specific IIABC components	SP0871	0.6	6.61E-05	conserved hypothetical protein
SP0910	2.1	4.07E-07	conserved hypothetical protein	SP0920	0.6	2.77E-05	carboxynorspermidine decarboxylase, <i>nspC</i>
SP0912	8.7	1.76E-12	ABC transporter, ATP-binding protein	SP0922	0.6	1.05E-05	carbon-nitrogen hydrolase family protein
SP0913	9.6	8.73E-11	putative ABC transporter, permease protein	SP1071	0.5	4.18E-05	ABC transporter, ATP-binding protein
SP1025	1.8	5.31E-05	hypothetical protein	SP1117	0.4	2.28E-06	DNA ligase, NAD-dependent, <i>ligA</i>
SP1148	1.9	7.03E-05	IS630-Spn1, transposase Orf2	SP1121	0.4	5.82E-06	hypothetical protein
SP1343	1.8	3.83E-06	prolyl oligopeptidase family protein	SP1122	0.5	9.90E-05	glucose-1-phosphate adenylyltransferase, <i>glgC</i>

<i>SP1344</i>	1.9	5.84E-06	conserved hypothetical protein	<i>SP1175</i>	0.5	2.17E-05	conserved domain protein
<i>SP1422</i>	1.7	9.79E-05	hypothetical protein	<i>SP1383</i>	0.3	7.29E-08	alanyl-tRNA synthetase, alaS
<i>SP1480</i>	1.8	8.38E-05	hypothetical protein	<i>SP1384</i>	0.5	9.53E-07	conserved hypothetical protein
<i>SP1588</i>	2.2	7.12E-07	oxidoreductase, pyridine nucleotide-disulfide, class I	<i>SP1441</i>	0.5	8.21E-07	IS66 family element, Orf3, degenerate
<i>SP1646</i>	1.6	9.41E-05	metallo-beta-lactamase superfamily protein	<i>SP1468</i>	0.6	7.97E-05	pyridoxine biosynthesis protein
<i>SP1648</i>	2.5	3.13E-08	manganese ABC transporter, ATP-binding protein, <i>psaB</i>	<i>SP1474</i>	0.5	1.25E-06	glycyl-tRNA synthetase, beta subunit, <i>glyS</i>
<i>SP1649</i>	2.6	1.51E-06	putative manganese ABC transporter, permease, <i>psaC</i>	<i>SP1477</i>	0.5	2.22E-06	hypothetical protein
<i>SP1674</i>	1.9	3.60E-06	putative phosphosugar-binding transcriptional regulator	<i>SP1531</i>	0.5	2.29E-05	hypothetical protein
<i>SP1683</i>	2.9	1.00E-07	sugar ABC transporter, sugar-binding protein	<i>SP1533</i>	0.5	3.19E-05	conserved domain protein
<i>SP1774</i>	2.2	4.56E-07	putative transcriptional regulator	<i>SP1576</i>	0.4	1.45E-07	homoserine O-succinyltransferase, <i>metA</i>
<i>SP1786</i>	3.0	6.80E-08	conserved hypothetical protein	<i>SP1577</i>	0.5	3.45E-05	adenine phosphoribosyltransferase, <i>apt</i>
<i>SP1787</i>	2.3	1.48E-06	hypothetical protein	<i>SP1630</i>	0.3	1.39E-08	hypothetical protein
<i>SP1854</i>	2.0	8.24E-05	galactose operon repressor, <i>galR</i>	<i>SP1631</i>	0.4	5.92E-08	threonyl-tRNA synthetase, <i>thrS</i>
<i>SP1885</i>	2.0	2.18E-05	trehalose operon transcriptional repressor, <i>treR</i>	<i>SP1651</i>	0.4	4.36E-06	thiol peroxidase, <i>psaD</i>
<i>SP2060</i>	1.9	1.26E-05	pyrrolidone-carboxylate peptidase, <i>pcp-2</i>	<i>SP1659</i>	0.4	1.10E-06	isoleucyl-tRNA synthetase
<i>SP2062</i>	2.0	6.08E-05	transcriptional regulator, MarR family	<i>SP1661</i>	0.6	1.10E-05	cell division protein DivIVA
<i>SP2063</i>	7.4	1.65E-10	LysM domain protein	<i>SP1673</i>	0.6	8.38E-06	penicillin-binding protein 2B, <i>penA</i>
<i>SP2084</i>	2.5	1.78E-07	phosphate ABC transporter, phosphate-binding protein, <i>pstS</i>	<i>SP1695</i>	0.6	2.52E-05	putative acetyl xylan esterase
<i>SP2086</i>	1.9	8.29E-05	phosphate ABC transporter, permease protein, <i>pstA</i>	<i>SP1743</i>	0.6	1.41E-05	conserved hypothetical protein
<i>SP2087</i>	2.1	1.52E-06	phosphate ABC transporter, ATP-binding protein, <i>pstB</i>	<i>SP1906</i>	0.6	3.89E-05	chaperonin, 60 kDa
<i>SP2088</i>	1.8	3.84E-05	phosphate transport system regulatory protein PhoU	<i>SP2026</i>	0.4	3.78E-06	alcohol dehydrogenase, iron-containing
<i>SP2136</i>	3.6	2.70E-09	choline binding protein <i>PcpA</i>	<i>SP2055</i>	0.5	1.12E-06	alcohol dehydrogenase, zinc-containing
<i>SP2197</i>	1.8	1.44E-05	putative ABC transporter, substrate-binding protein	<i>SP2134</i>	0.6	2.65E-05	ribosomal protein L32, <i>rpmF</i>
<i>SP2199</i>	1.9	1.28E-05	conserved hypothetical protein	<i>SP2188</i>	0.6	3.03E-05	chaperonin, 33 kDa, <i>hslO</i>

				<i>SP2189</i>	0.6	3.81E-05	putative TIM-barrel protein, NifR3 family
				<i>SP2239</i>	0.5	2.84E-05	serine protease
				<i>SP2240</i>	0.5	7.31E-05	spspoJ protein

1

2 C. List of genes differentially expressed upon **15 min.** treatment with **nisin**:

up-regulated genes				down-regulated genes			
Gene ID	Ratio	Bayes.p	NCBI annotation	Gene ID	Ratio	Bayes.p	NCBI annotation
<i>SP0185</i>	1.3	7.81E-04	magnesium transporter, CorA family	<i>SP0229</i>	0.8	6.51E-04	ribosomal protein L15, <i>rplO</i>
<i>SP0335</i>	1.4	2.99E-05	cell division protein FtsL	<i>SP0230</i>	0.7	7.11E-05	preprotein translocase, SecY subunit, <i>secY</i>
<i>SP0415</i>	1.4	5.77E-05	enoyl-CoA hydratase/isomerase family protein	<i>SP0237</i>	0.7	2.26E-04	ribosomal protein L17, <i>rplQ</i>
<i>SP0416</i>	1.3	5.09E-04	transcriptional regulator, MarR family	<i>SP0285</i>	0.7	1.32E-04	alcohol dehydrogenase, zinc-containing
<i>SP0641</i>	1.3	2.33E-04	serine protease, subtilase family	<i>SP0366</i>	0.7	8.16E-05	oligopeptide ABC transporter, oligopeptide-binding protein AliA
<i>SP0664</i>	1.3	5.63E-04	zinc metalloprotease ZmpB	<i>SP0441</i>	0.6	6.31E-06	ribosomal protein L28
<i>SP0851</i>	1.5	7.05E-05	conserved hypothetical protein	<i>SP0501</i>	0.5	3.15E-06	transcriptional regulator, MerR family
<i>SP0875</i>	1.6	1.01E-05	lactose phosphotransferase system repressor	<i>SP0502</i>	0.5	6.55E-05	glutamine synthetase, type I
<i>SP0876</i>	1.7	2.56E-06	putative 1-phosphofructokinase	<i>SP0557</i>	0.7	3.17E-04	ribosome-binding factor A, <i>rbfA</i>
<i>SP0912</i>	9.1	1.40E-12	ABC transporter, ATP-binding protein	<i>SP0577</i>	0.6	2.84E-06	PTS system, beta-glucosides-specific IIBC omponents
<i>SP0913</i>	13.3	5.84E-13	putative ABC transporter, permease protein	<i>SP0578</i>	0.6	3.17E-06	6-phospho-beta-glucosidase, <i>bglA-2</i>
<i>SP0914</i>	1.6	6.77E-05	nodulin-related protein, truncation	<i>SP0645</i>	0.6	1.06E-05	putative PTS system IIA component
<i>SP1178</i>	1.3	3.08E-04	NrdH-redoxin	<i>SP0670</i>	0.7	1.46E-04	hypothetical protein
<i>SP1343</i>	1.3	5.41E-04	prolyl oligopeptidase family protein	<i>SP0731</i>	0.7	1.24E-04	conserved domain protein
<i>SP1578</i>	1.4	6.75E-04	putative methyltransferase	<i>SP0838</i>	0.7	1.87E-04	ribosomal protein S20, <i>rpsT</i>
<i>SP1588</i>	1.3	6.36E-04	oxidoreductase, pyridine nucleotide-disulfide, class I	<i>SP0922</i>	0.7	2.84E-04	carbon-nitrogen hydrolase family protein
<i>SP1871</i>	1.6	5.99E-04	iron-compound ABC transporter, ATP-binding protein	<i>SP0962</i>	0.8	5.53E-04	lactoylglutathione lyase, <i>gloA</i>

<i>SP1872</i>	1.6	2.74E-04	iron-compound ABC transporter, iron-compound-binding protein	<i>SP1080</i>	0.7	1.91E-04	hypothetical protein
<i>SP2173</i>	1.3	7.90E-04	dltD protein	<i>SP1187</i>	0.6	7.24E-06	transcription antiterminator LacT
<i>SP2216</i>	1.5	5.33E-04	secreted 45 kd protein, <i>usp45</i>	<i>SP1220</i>	0.8	4.62E-04	L-lactate dehydrogenase
				<i>SP1241</i>	0.5	6.49E-06	acid ABC transporter, amino acid-binding protein/permease protein
				<i>SP1242</i>	0.5	8.46E-07	amino acid ABC transporter, ATP-binding protein
				<i>SP1295</i>	0.7	2.10E-04	crcB protein
				<i>SP1297</i>	0.6	5.88E-05	flavodoxin
				<i>SP1306</i>	0.6	7.98E-06	NADP-specific glutamate dehydrogenase, <i>gdhA</i>
				<i>SP1354</i>	0.7	8.63E-05	ribosomal protein L7/L12, <i>rplL</i>
				<i>SP1394</i>	0.8	8.82E-04	amino acid ABC transporter, amino acid-binding protein
				<i>SP1414</i>	0.8	5.80E-04	ribosomal protein S21, <i>rpsU</i>
				<i>SP1499</i>	0.7	2.18E-04	bacterocin transport accessory protein
				<i>SP1507</i>	0.7	1.06E-04	ATP synthase F1, epsilon subunit, <i>atpC</i>
				<i>SP1531</i>	0.7	1.38E-04	hypothetical protein
				<i>SP1648</i>	0.7	3.46E-04	manganese ABC transporter, ATP-binding protein, <i>psaB</i>
				<i>SP1649</i>	0.8	2.98E-04	putative manganese ABC transporter, permease, <i>psaC</i>
				<i>SP1864</i>	0.7	3.17E-04	conserved hypothetical protein
				<i>SP1959</i>	0.7	2.25E-04	nucleoside diphosphate kinase
				<i>SP1970</i>	0.7	1.90E-04	aspartate--ammonia ligase, <i>asnA</i>
				<i>SP1996</i>	0.7	9.24E-05	universal stress protein family
				<i>SP2055</i>	0.7	5.72E-04	alcohol dehydrogenase, zinc-containing
				<i>SP2108</i>	0.7	6.14E-04	maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein, <i>malX</i>
				<i>SP2126</i>	0.7	3.78E-04	dihydroxy-acid dehydratase, <i>ilvD</i>

1

2 **D.** List of genes differentially expressed upon **30 min.** treatment with **nisin**:

up-regulated genes	down-regulated genes
--------------------	----------------------

Gene ID	Ratio	Bayes.p	NCBI annotation	Gene ID	Ratio	Bayes.p	NCBI annotation
<i>SP0148</i>	1.6	4.09E-04	ABC transporter, substrate-binding protein	<i>SP0496</i>	0.7	4.22E-04	Na/Pi cotransporter II-related protein
<i>SP0415</i>	2.0	6.16E-04	enoyl-CoA hydratase/isomerase family protein	<i>SP0501</i>	0.4	1.54E-06	transcriptional regulator, MerR family
<i>SP0419</i>	2.0	5.08E-04	enoyl-(acyl-carrier-protein) reductase	<i>SP0502</i>	0.5	5.47E-06	glutamine synthetase, type I
<i>SP0422</i>	2.2	1.62E-04	3-oxoacyl-(acyl-carrier-protein) synthase II, <i>fabF</i>	<i>SP1160</i>	0.5	1.14E-04	putative lipoate-protein ligase
<i>SP0875</i>	1.5	8.49E-04	lactose phosphotransferase system repressor	<i>SP1241</i>	0.6	1.55E-04	acid ABC transporter, amino acid-binding protein/permease protein
<i>SP0876</i>	1.6	3.68E-05	putative 1-phosphofructokinase	<i>SP1242</i>	0.6	4.04E-05	amino acid ABC transporter, ATP-binding protein
<i>SP0912</i>	6.0	4.38E-09	ABC transporter, ATP-binding protein	<i>SP1648</i>	0.6	1.26E-05	manganese ABC transporter, ATP-binding protein, <i>psaB</i>
<i>SP0913</i>	11.9	4.14E-12	putative ABC transporter, permease protein	<i>SP1649</i>	0.6	2.09E-05	putative manganese ABC transporter, permease, <i>psaC</i>
<i>SP1588</i>	1.8	3.89E-06	oxidoreductase, pyridine nucleotide-disulfide, class I	<i>SP1664</i>	0.7	7.90E-04	<i>ylmF</i> protein
<i>SP1869</i>	1.7	3.36E-04	iron-compound ABC transporter, permease protein	<i>SP2136</i>	0.6	2.62E-05	choline binding protein <i>PcpA</i>
<i>SP1870</i>	2.5	7.42E-06	iron-compound ABC transporter, permease protein				
<i>SP1871</i>	1.9	3.85E-04	iron-compound ABC transporter, ATP-binding protein				
<i>SP1872</i>	1.8	5.11E-04	iron-compound ABC transporter, iron-compound-binding protein				
<i>SP2062</i>	1.6	7.32E-04	transcriptional regulator, MarR family				
<i>SP2063</i>	1.9	1.29E-04	LysM domain protein				

1

2 E. List of genes differentially expressed upon **15 min.** treatment with **LL-37**:

up-regulated genes				down-regulated genes			
Gene ID	Ratio	Bayes.p	NCBI annotation	Gene ID	Ratio	Bayes.p	NCBI annotation

<i>SP0001</i>	1.4	5.73E-05	chromosomal replication initiator protein DnaA	<i>SP0004</i>	0.8	1.14E-04	GTP-binding protein
<i>SP0055</i>	1.3	3.16E-04	Hypothetical protein	<i>SP0008</i>	0.8	6.32E-04	Hypothetical protein
<i>SP0056</i>	1.3	9.36E-04	adenylosuccinate lyase	<i>SP0024</i>	0.6	1.47E-07	conserved hypothetical protein
<i>SP0071</i>	1.5	6.03E-04	zinc metalloprotease ZmpC	<i>SP0025</i>	0.8	3.97E-04	Hypothetical protein
<i>SP0088</i>	1.5	3.08E-06	Hypothetical protein	<i>SP0026</i>	0.6	1.59E-06	Hypothetical protein
<i>SP0089</i>	1.4	4.89E-04	Hypothetical protein	<i>SP0027</i>	0.8	2.71E-05	ribose-phosphate pyrophosphokinase
<i>SP0157</i>	1.7	5.99E-08	Hypothetical protein	<i>SP0032</i>	0.8	2.69E-04	DNA polymerase I
<i>SP0185</i>	1.3	1.99E-04	magnesium transporter, CorA family	<i>SP0034</i>	0.6	3.56E-06	membrane protein
<i>SP0192</i>	1.4	2.66E-05	conserved hypothetical protein	<i>SP0083</i>	0.8	2.37E-04	DNA-binding response regulator
<i>SP0194</i>	1.3	2.28E-04	conserved hypothetical protein	<i>SP0084</i>	0.7	1.55E-05	sensor histidine kinase
<i>SP0197</i>	1.5	2.94E-06	putative dihydrofolate synthetase	<i>SP0090</i>	0.7	9.96E-04	ABC transporter, permease protein
<i>SP0200</i>	1.3	2.98E-04	competence-induced protein Ccs4	<i>SP0107</i>	0.7	4.81E-04	LysM domain protein
<i>SP0234</i>	1.3	7.21E-04	ribosomal protein S13	<i>SP0117</i>	0.5	4.76E-06	pneumococcal surface protein A
<i>SP0237</i>	1.7	5.03E-07	ribosomal protein L17	<i>SP0202</i>	0.8	6.88E-04	anaerobic ribonucleoside-triphosphate reductase
<i>SP0261</i>	1.5	8.59E-06	undecaprenyl diphosphate synthase	<i>SP0238</i>	0.6	6.26E-05	ACT domain protein
<i>SP0279</i>	1.4	1.81E-04	conserved hypothetical protein	<i>SP0239</i>	0.7	1.24E-04	conserved hypothetical protein
<i>SP0369</i>	1.8	2.06E-08	penicillin-binding protein 1A	<i>SP0255</i>	0.7	2.13E-04	acetyltransferase, GNAT family
<i>SP0370</i>	1.9	2.72E-07	recombination protein U	<i>SP0268</i>	0.7	2.16E-04	putative alkaline amylopullulanase
<i>SP0372</i>	1.5	3.00E-05	conserved hypothetical protein	<i>SP0281</i>	0.7	7.96E-06	aminopeptidase C
<i>SP0374</i>	1.3	4.46E-04	hypothetical protein	<i>SP0282</i>	0.3	1.84E-10	PTS system, mannose-specific IID component
<i>SP0385</i>	1.5	2.64E-06	conserved hypothetical protein	<i>SP0283</i>	0.2	9.42E-11	PTS system, mannose-specific IIC component
<i>SP0386</i>	1.5	1.55E-06	putative sensor histidine kinase	<i>SP0284</i>	0.2	1.37E-11	PTS system, mannose-specific IIAB components
<i>SP0402</i>	1.4	1.40E-05	signal peptidase I	<i>SP0285</i>	0.7	2.08E-05	alcohol dehydrogenase, zinc-containing
<i>SP0403</i>	1.3	1.16E-04	ribonuclease HIII	<i>SP0287</i>	0.5	1.94E-07	xanthine/uracil permease family protein
<i>SP0404</i>	1.4	2.32E-05	hypothetical protein	<i>SP0289</i>	0.7	8.87E-04	dihydropteroate synthase
<i>SP0405</i>	1.5	9.89E-06	conserved hypothetical protein	<i>SP0290</i>	0.7	6.65E-06	dihydrofolate synthetase
<i>SP0406</i>	1.2	7.50E-04	MutS2 family protein	<i>SP0291</i>	0.7	6.09E-05	GTP cyclohydrolase I
<i>SP0408</i>	1.9	1.20E-06	sodium:alanine symporter family protein	<i>SP0292</i>	0.7	7.31E-04	bifunctional folate synthesis protein
<i>SP0415</i>	1.5	1.30E-05	enoyl-CoA hydratase/isomerase family protein	<i>SP0293</i>	0.7	7.63E-05	hypothetical protein
<i>SP0416</i>	1.3	3.65E-04	transcriptional regulator, MarR family	<i>SP0303</i>	0.6	1.59E-04	6-phospho-beta-glucosidase
<i>SP0417</i>	1.5	6.68E-06	3-oxoacyl-(acyl-carrier-protein) synthase	<i>SP0341</i>	0.8	9.71E-05	hypothetical protein

			III				
<i>SP0419</i>	1.4	4.10E-05	enoyl-(acyl-carrier-protein) reductase	<i>SP0366</i>	0.3	1.28E-11	oligopeptide ABC transporter AliA
<i>SP0424</i>	1.3	2.28E-04	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase, <i>fabZ</i>	<i>SP0413</i>	0.7	1.03E-05	aspartate kinase
<i>SP0427</i>	1.4	9.15E-06	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit, <i>accA</i>	<i>SP0445</i>	0.7	1.73E-04	acetolactate synthase, large subunit, biosynthetic type, <i>ilvB</i>
<i>SP0457</i>	1.3	2.79E-05	bacitracin resistance protein, <i>bacA</i>	<i>SP0446</i>	0.6	1.08E-06	acetolactate synthase, small subunit, <i>ilvN</i>
<i>SP0496</i>	1.5	2.39E-06	Na/Pi cotransporter II-related protein	<i>SP0447</i>	0.6	4.01E-06	ketol-acid reductoisomerase, <i>ilvC</i>
<i>SP0499</i>	1.4	8.94E-05	phosphoglycerate kinase	<i>SP0448</i>	0.7	9.48E-05	hypothetical protein
<i>SP0501</i>	3.1	1.52E-10	transcriptional regulator, MerR family	<i>SP0450</i>	0.7	4.78E-05	threonine dehydratase, <i>ilvA</i>
<i>SP0502</i>	2.9	8.33E-11	glutamine synthetase, type I	<i>SP0459</i>	0.7	2.31E-06	formate acetyltransferase
<i>SP0503</i>	2.7	3.04E-07	hypothetical protein	<i>SP0477</i>	0.7	1.66E-04	6-phospho-beta-galactosidase, <i>lacG</i> -1
<i>SP0504</i>	1.9	7.65E-07	hypothetical protein	<i>SP0479</i>	0.8	0.000731	potassium uptake protein, Trk family
<i>SP0524</i>	2.0	6.40E-07	BlpT protein, fusion	<i>SP0516</i>	0.6	8.99E-07	heat shock protein GrpE
<i>SP0525</i>	1.6	6.11E-07	BlpS protein	<i>SP0517</i>	0.6	8.46E-08	DnaK protein
<i>SP0526</i>	1.4	6.28E-05	response regulator BlpR	<i>SP0518</i>	0.7	1.69E-06	hypothetical protein
<i>SP0527</i>	1.4	8.55E-05	putative sensor histidine kinase BlpH	<i>SP0519</i>	0.8	5.08E-04	dnaJ protein
<i>SP0529</i>	1.7	8.10E-07	BlpB ABC transporter	<i>SP0565</i>	0.7	5.87E-04	conserved domain protein
<i>SP0530</i>	3.4	1.53E-09	BlpA ABC transporter	<i>SP0566</i>	0.7	1.25E-04	acetyltransferase, GNAT family
<i>SP0533</i>	1.5	3.41E-05	bacteriocin BlpK	<i>SP0568</i>	0.7	2.55E-06	valyl-tRNA synthetase, <i>valS</i>
			immunity protein BlpY	<i>SP0577</i>	0.4	2.45E-06	PTS system, beta-glucosides-specific
<i>SP0545</i>	5.1	6.74E-12		<i>SP0578</i>	0.3	1.38E-06	IIABC components
<i>SP0546</i>	3.5	5.96E-09	BlpZ protein, fusion				6-phospho-beta-glucosidase
			conserved domain protein	<i>SP0579</i>	0.7	8.16E-06	phenylalanyl-tRNA synthetase, alpha subunit, <i>pheS</i>
<i>SP0547</i>	3.7	6.53E-10		<i>SP0581</i>	0.8	3.65E-04	phenylalanyl-tRNA synthetase, beta subunit, <i>pheT</i>
<i>SP0552</i>	1.3	9.69E-04	SP14.3 protein				single-stranded-DNA-specific exonuclease RecJ
<i>SP0553</i>	1.2	7.22E-04	N utilization substance protein A, <i>nusA</i>	<i>SP0611</i>	0.8	1.09E-04	HIT family protein
<i>SP0556</i>	1.2	9.61E-04	translation initiation factor IF-2, <i>infB</i>	<i>SP0628</i>	0.7	5.49E-05	membrane protein
<i>SP0557</i>	1.6	2.37E-05	ribosome-binding factor A, <i>rbfA</i>	<i>SP0637</i>	0.8	3.79E-04	conserved hypothetical protein
<i>SP0582</i>	1.6	3.96E-06	hypothetical protein	<i>SP0638</i>	0.8	1.06E-04	pyruvate oxidase
<i>SP0587</i>	1.6	4.17E-04	hypothetical protein	<i>SP0730</i>	0.5	7.37E-08	conserved domain protein
<i>SP0588</i>	1.2	4.09E-04	polyribonucleotide nucleotidyltransferase	<i>SP0731</i>	0.5	8.12E-08	mannose-6-phosphate isomerase, <i>manA</i>
<i>SP0589</i>	1.3	1.19E-04	serine acetyltransferase, <i>cysE</i>	<i>SP0736</i>	0.7	5.05E-04	PTS system, IIABC components
<i>SP0590</i>	1.3	1.03E-04	acetyltransferase, GNAT family	<i>SP0758</i>	0.7	9.57E-05	

<i>SP0591</i>	1.3	3.64E-04	cysteinyl-tRNA synthetase	<i>SP0770</i>	0.7	1.67E-04	ABC transporter, ATP-binding protein
<i>SP0592</i>	1.4	3.76E-05	conserved hypothetical protein	<i>SP0775</i>	0.7	7.38E-05	ribosomal protein S16
<i>SP0593</i>	1.4	6.12E-06	leucine-rich protein	<i>SP0845</i>	0.5	2.03E-07	lipoprotein
<i>SP0617</i>	2.0	6.43E-08		<i>SP0887</i>	0.7	1.76E-05	putative type I restriction-modification system, S subunit
<i>SP0742</i>	1.8	2.78E-07	conserved domain protein	<i>SP0916</i>	0.6	1.01E-04	lysine decarboxylase
<i>SP0748</i>	1.3	4.73E-04	conserved hypothetical protein	<i>SP0918</i>	0.6	5.49E-06	spermidine synthase, <i>speE</i>
<i>SP0762</i>	1.7	2.06E-07	S-adenosylmethionine synthetase	<i>SP0919</i>	0.5	1.21E-07	conserved hypothetical protein
<i>SP0783</i>	2.6	5.87E-09	conserved hypothetical protein	<i>SP0920</i>	0.5	9.91E-09	carboxynorspermidine decarboxylase
<i>SP0785</i>	4.1	6.34E-12	conserved hypothetical protein	<i>SP0921</i>	0.5	1.98E-08	conserved hypothetical protein
			ABC transporter, ATP-binding protein				carbon-nitrogen hydrolase family protein
<i>SP0786</i>	5.1	2.73E-12		<i>SP0922</i>	0.5	1.09E-05	
<i>SP0787</i>	4.6	1.76E-11	conserved hypothetical protein	<i>SP1013</i>	0.7	4.82E-05	aspartate-semialdehyde dehydrogenase
			conserved hypothetical protein				iron-compound ABC transporter, iron compound-binding protein
<i>SP0789</i>	1.6	8.25E-06		<i>SP1032</i>	0.5	8.37E-09	iron-compound ABC transporter, permease protein
			conserved domain protein	<i>SP1033</i>	0.7	2.11E-04	iron-compound ABC transporter, permease protein
<i>SP0790</i>	1.5	9.27E-06		<i>SP1034</i>	0.6	2.13E-07	iron-compound ABC transporter, ATP-binding protein
<i>SP0798</i>	2.5	2.80E-10	DNA-binding response regulator CiaR				hypothetical protein
				<i>SP1035</i>	0.5	7.59E-09	
<i>SP0799</i>	2.4	4.81E-09		<i>SP1036</i>	0.6	5.52E-04	putative type II restriction endonuclease
<i>SP0800</i>	1.5	1.41E-05	hypothetical protein				
			hydrolase, haloacid dehalogenase-like family	<i>SP1037</i>	0.8	2.89E-04	hypothetical protein
<i>SP0805</i>	1.5	2.10E-06		<i>SP1038</i>	0.8	2.63E-04	hypothetical protein
<i>SP0829</i>	1.3	1.34E-04	Phosphopentomutase, <i>deoB</i>	<i>SP1039</i>	0.6	5.65E-06	site-specific recombinase, resolvase family
<i>SP0846</i>	1.3	9.65E-04	sugar ABC transporter, ATP-binding protein				hypothetical protein
			conserved hypothetical protein	<i>SP1040</i>	0.6	1.23E-06	conserved hypothetical protein
<i>SP0851</i>	1.4	3.10E-04		<i>SP1041</i>	0.6	1.31E-05	
<i>SP0861</i>	1.6	1.60E-04	hypothetical protein				
			lactose phosphotransferase system	<i>SP1069</i>	0.7	9.57E-05	conserved hypothetical protein
<i>SP0875</i>	1.7	3.98E-04	repressor	<i>SP1070</i>	0.7	2.68E-04	ABC transporter, ATP-binding protein
<i>SP0876</i>	1.8	9.06E-04	putative 1-phosphofructokinase	<i>SP1114</i>	0.8	6.85E-05	glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent, <i>gapN</i>
<i>SP0877</i>	2.3	5.20E-06	SpoE family protein				hypothetical protein
			hypothetical protein	<i>SP1119</i>	0.6	1.09E-05	
<i>SP0878</i>	1.5	1.35E-06					
			putative type I restriction-modification system, R subunit	<i>SP1127</i>	0.7	3.88E-04	enolase
<i>SP0895</i>	1.3	2.86E-05		<i>SP1128</i>	0.7	7.45E-05	
<i>SP0904</i>	1.3	8.86E-05	conserved hypothetical protein				

<i>SP0905</i>	1.3	2.95E-04	conserved hypothetical protein	<i>SP1170</i>	0.7	4.48E-05	hypothetical protein
<i>SP0910</i>	1.3	2.26E-04	conserved hypothetical protein	<i>SP1171</i>	0.7	4.22E-05	hydrolase, haloacid dehalogenase-like family
<i>SP0913</i>	1.9	3.39E-05	putative ABC transporter, permease protein	<i>SP1175</i>	0.7	2.83E-04	conserved domain protein
<i>SP0925</i>	1.5	1.08E-04	conserved hypothetical protein	<i>SP1185</i>	0.6	1.44E-05	PTS system, lactose-specific IIBC components, lacE-2
<i>SP0928</i>	1.2	9.44E-04	signal peptidase II, <i>lspA</i>	<i>SP1186</i>	0.5	1.85E-05	PTS system, lactose-specific IIA component, lacF-2
<i>SP0956</i>	1.4	8.82E-04	hypothetical protein	<i>SP1187</i>	0.5	2.75E-06	transcription antiterminator LacT
<i>SP0957</i>	1.9	3.00E-07	ABC transporter, ATP-binding protein	<i>SP1190</i>	0.7	1.55E-04	tagatose 1,6-diphosphate aldolase, <i>lacD</i>
<i>SP0958</i>	2.0	3.52E-07	hypothetical protein	<i>SP1191</i>	0.7	7.79E-04	tagatose-6-phosphate kinase, <i>lacC</i>
<i>SP0974</i>	1.4	9.61E-04	putative preprotein translocase, SecG subunit	<i>SP1192</i>	0.7	1.86E-05	galactose-6-phosphate isomerase, LacB subunit, <i>lacB</i>
<i>SP0975</i>	1.5	1.41E-05	exoribonuclease, VacB/Rnb family	<i>SP1193</i>	0.7	2.98E-04	galactose-6-phosphate isomerase, LacA subunit, <i>lacA</i>
<i>SP0976</i>	1.5	5.13E-06	SsrA-binding protein"	<i>SP1212</i>	0.7	1.97E-05	tRNA pseudouridine synthase B, <i>truB</i>
<i>SP0977</i>	1.6	4.65E-06	tellurite resistance protein TehB	<i>SP1263</i>	0.6	7.02E-04	DNA topoisomerase I, topA
<i>SP0981</i>	1.3	1.88E-04	putative protease maturation protein	<i>SP1298</i>	0.6	1.06E-08	DHH subfamily 1 protein
<i>SP0987</i>	1.3	2.31E-04	hypothetical protein	<i>SP1339</i>	0.7	1.88E-04	hypothetical protein
<i>SP1023</i>	1.3	5.22E-04	acetyltransferase, GNAT family	<i>SP1345</i>	0.7	2.59E-04	hypothetical protein
<i>SP1024</i>	1.2	8.22E-04	serine hydroxymethyltransferase, <i>glyA</i>	<i>SP1383</i>	0.8	3.04E-04	alanyl-tRNA synthetase, <i>alaS</i>
<i>SP1027</i>	3.3	8.31E-11	conserved hypothetical protein	<i>SP1395</i>	0.7	2.98E-05	putative phosphate transport system regulatory protein PhoU
<i>SP1029</i>	1.7	9.81E-08	RNA methyltransferase, TrmA family	<i>SP1396</i>	0.8	1.57E-04	putative phosphate ABC transporter, ATP-binding protein
<i>SP1075</i>	1.7	2.37E-08	glycosyl transferase CpoA	<i>SP1397</i>	0.8	9.47E-04	putative phosphate ABC transporter, ATP-binding protein
<i>SP1076</i>	1.4	1.44E-05	glycosyl transferase, group 1	<i>SP1398</i>	0.8	5.64E-04	putative phosphate ABC transporter, permease protein
<i>SP1077</i>	1.6	1.07E-06	conserved domain protein	<i>SP1445</i>	0.6	1.94E-07	GMP synthase, guaA
<i>SP1082</i>	1.2	8.51E-04	acetyltransferase, GNAT family	<i>SP1455</i>	0.7	2.75E-04	hypothetical protein
<i>SP1093</i>	1.3	7.51E-04	hypothetical protein	<i>SP1461</i>	0.8	7.33E-04	amino acid ABC transporter, permease protein
<i>SP1148</i>	1.5	1.88E-05	IS630-Spn1, transposase Orf2	<i>SP1462</i>	0.7	8.06E-06	conserved hypothetical protein
<i>SP1149</i>	1.4	2.97E-05	IS630-Spn1, transposase Orf1	<i>SP1463</i>	0.6	5.93E-07	methylated-DNA--protein-cysteine S-methyltransferase
<i>SP1151</i>	1.4	8.54E-05	exonuclease RexB	<i>SP1464</i>	0.6	1.05E-06	acetyltransferase, GNAT family

<i>SP1161</i>	1.4	9.15E-04	putative acetoin dehydrogenase complex, E3 component, dihydroliipoamide dehydrogenase	<i>SP1468</i>	0.7	9.65E-05	pyridoxine biosynthesis protein
<i>SP1162</i>	1.3	7.77E-04	putative acetoin dehydrogenase complex, E2 component, dihydroliipoamide acetyltransferase	<i>SP1469</i>	0.8	5.21E-04	NADH oxidase
<i>SP1229</i>	1.3	2.74E-04	formate--tetrahydrofolate ligase	<i>SP1491</i>	0.7	1.75E-05	putative glycerol uptake facilitator protein
<i>SP1241</i>	2.4	2.27E-09	amino acid ABC transporter, amino acid-binding protein/permease protein	<i>SP1500</i>	0.7	1.42E-04	amino acid ABC transporter, amino acid-binding protein
<i>SP1242</i>	2.7	1.23E-09	amino acid ABC transporter, ATP-binding protein	<i>SP1507</i>	0.6	4.79E-06	ATP synthase F1, epsilon subunit, <i>atpC</i>
<i>SP1243</i>	1.5	3.09E-06	glucose-6-phosphate 1-dehydrogenase, <i>zwf</i>	<i>SP1508</i>	0.6	4.11E-07	ATP synthase F1, beta subunit, <i>atpD</i>
<i>SP1260</i>	1.3	3.36E-04	copper homeostasis protein CutC	<i>SP1509</i>	0.6	2.36E-08	ATP synthase F1, gamma subunit, <i>atpG</i>
<i>SP1261</i>	1.3	7.39E-04	conserved hypothetical protein	<i>SP1510</i>	0.6	3.47E-08	ATP synthase F1, alpha subunit, <i>atpA</i>
<i>SP1283</i>	1.5	2.81E-06	heat shock protein HtpX	<i>SP1511</i>	0.6	1.31E-07	ATP synthase F1, delta subunit, <i>atpH</i>
<i>SP1284</i>	1.3	4.00E-04	lemA protein	<i>SP1512</i>	0.6	5.14E-08	ATP synthase F0, B subunit, <i>atpF</i>
<i>SP1299</i>	1.3	8.50E-04	ribosomal protein L31, <i>rpmE</i>	<i>SP1513</i>	0.6	1.44E-07	ATP synthase F0, A subunit, <i>atpB</i>
<i>SP1305</i>	1.8	1.13E-04	hypothetical protein	<i>SP1517</i>	0.8	5.46E-04	transcription elongation factor GreA
<i>SP1306</i>	1.7	3.03E-07	NADP-specific glutamate dehydrogenase, <i>gdhA</i>	<i>SP1533</i>	0.8	7.19E-05	conserved domain protein
<i>SP1315</i>	1.3	1.20E-04	v-type sodium ATP synthase, subunit D	<i>SP1534</i>	0.8	5.84E-05	inorganic pyrophosphatase, manganese-dependent, <i>ppaC</i>
<i>SP1378</i>	1.3	7.95E-04	conserved hypothetical protein	<i>SP1540</i>	0.8	2.83E-04	single-strand binding protein
<i>SP1380</i>	1.3	2.64E-04	hypothetical protein	<i>SP1548</i>	0.7	2.81E-06	hypothetical protein
<i>SP1381</i>	1.5	1.08E-04	ABC transporter, ATP-binding protein	<i>SP1549</i>	0.6	1.21E-05	polypeptide deformylase, <i>def-2</i>
<i>SP1405</i>	1.4	2.67E-05	conserved hypothetical protein	<i>SP1574</i>	0.8	2.65E-04	triosephosphate isomerase
<i>SP1422</i>	1.4	5.19E-04	hypothetical protein	<i>SP1576</i>	0.8	6.73E-04	homoserine O-succinyltransferase, <i>metaA</i>
<i>SP1424</i>	1.4	7.12E-04	hypothetical protein	<i>SP1578</i>	0.6	3.23E-04	putative methyltransferase
<i>SP1479</i>	1.3	1.71E-04	peptidoglycan N-acetylglucosamine deacetylase A, <i>pgdA</i>	<i>SP1580</i>	0.4	8.68E-11	sugar ABC transporter, ATP-binding protein, <i>msmK</i>
<i>SP1529</i>	1.2	5.91E-04	putative polysaccharide biosynthesis protein	<i>SP1605</i>	0.7	3.44E-06	ferredoxin
<i>SP1546</i>	1.7	3.42E-07	conserved domain protein	<i>SP1607</i>	0.8	7.62E-04	UDP-glucose 4-epimerase, <i>galE-1</i>
<i>SP1560</i>	1.4	6.45E-05	conserved hypothetical protein	<i>SP1644</i>	0.7	3.68E-04	conserved hypothetical protein
<i>SP1561</i>	1.5	3.64E-06	conserved hypothetical protein	<i>SP1645</i>	0.7	2.36E-06	GTP pyrophosphokinase, <i>relA</i>
<i>SP1562</i>	1.3	4.88E-04	hypothetical protein	<i>SP1647</i>	0.7	6.36E-06	endopeptidase O, <i>pepO</i>
<i>SP1623</i>	1.3	3.01E-04	cation-transporting ATPase, E1-E2 family	<i>SP1659</i>	0.8	1.15E-04	isoleucyl-tRNA synthetase, <i>ileS</i>
<i>SP1625</i>	1.4	1.83E-04	putative cadmium resistance transporter	<i>SP1684</i>	0.7	1.64E-04	PTS system, IIBC components

<i>SP1636</i>	1.4	2.17E-05	Rrf2 family protein	<i>SP1685</i>	0.7	4.44E-05	conserved hypothetical protein
<i>SP1640</i>	1.6	3.03E-06	hypothetical protein	<i>SP1709</i>	0.6	4.14E-08	phosphoglycerate dehydrogenase-related protein
<i>SP1641</i>	1.4	1.02E-04	conserved domain protein	<i>SP1710</i>	0.7	4.85E-05	nitroreductase family protein
<i>SP1668</i>	1.4	2.71E-05	hypothetical protein	<i>SP1711</i>	0.7	2.38E-06	primosomal protein DnaI
<i>SP1669</i>	1.4	1.46E-05	MutT/nudix family protein	<i>SP1712</i>	0.7	5.36E-06	hypothetical protein
			UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase, <i>murF</i>	<i>SP1713</i>	0.7	5.66E-05	conserved hypothetical protein
<i>SP1670</i>	1.4	1.85E-05		<i>SP1716</i>	0.7	5.18E-05	conserved hypothetical protein
<i>SP1671</i>	1.5	4.46E-06	D-alanine--D-alanine ligase, <i>ddlA</i>	<i>SP1717</i>	0.5	5.03E-07	ABC transporter, ATP-binding protein
			putative phosphosugar-binding	<i>SP1778</i>	0.7	5.53E-06	aquaporin
<i>SP1674</i>	1.3	5.73E-04	transcriptional regulator				tryptophan synthase, alpha subunit, <i>trpA</i>
<i>SP1695</i>	2.9	6.32E-10	putative acetyl xylan esterase	<i>SP1811</i>	0.4	4.06E-08	tryptophan synthase, beta subunit, <i>trpB</i>
			hypothetical protein	<i>SP1812</i>	0.5	3.48E-06	N-(5'-phosphoribosyl)-anthranilate isomerase, <i>trpF</i>
<i>SP1696</i>	2.8	2.01E-09		<i>SP1813</i>	0.6	5.79E-06	anthranilate phosphoribosyltransferase, <i>trpD</i>
<i>SP1714</i>	7.2	1.63E-12	transcriptional regulator, GntR family	<i>SP1815</i>	0.6	3.52E-05	anthranilate synthase component II, <i>trpG</i>
			ABC transporter, ATP-binding protein	<i>SP1816</i>	0.5	2.01E-06	anthranilate synthase component I, <i>trpE</i>
<i>SP1715</i>	11.4	3.27E-13		<i>SP1817</i>	0.5	4.71E-05	ABC transporter, substrate-binding protein
			rRNA methyltransferase RsmB	<i>SP1826</i>	0.7	2.63E-04	oligopeptide ABC transporter, ATP-binding protein AmiE
<i>SP1734</i>	1.3	3.07E-04	conserved hypothetical protein	<i>SP1888</i>	0.8	3.17E-04	oligopeptide ABC transporter, oligopeptide-binding protein AmiA
<i>SP1750</i>	1.3	1.31E-04		<i>SP1891</i>	0.7	2.04E-06	chaperonin, 60 kDa, <i>groEL</i>
<i>SP1752</i>	1.4	1.99E-05	putative mechanosensitive ion channel	<i>SP1906</i>	0.7	2.53E-05	chaperonin, 10 kDa, <i>groES</i>
<i>SP1754</i>	1.4	4.47E-05	conserved hypothetical protein	<i>SP1907</i>	0.7	1.46E-04	hypothetical protein
			putative transcriptional regulator	<i>SP1915</i>	0.7	8.18E-04	IS1381, transposase OrfB
<i>SP1774</i>	1.4	1.92E-05		<i>SP1928</i>	0.8	1.94E-04	putative transcriptional regulator
			thioredoxin	<i>SP1942</i>	0.8	1.45E-04	acetyltransferase, GNAT family
<i>SP1776</i>	1.5	3.63E-04		<i>SP1943</i>	0.8	1.06E-04	DNA-directed RNA polymerase, beta' subunit
<i>SP1786</i>	1.5	4.65E-06	conserved hypothetical protein	<i>SP1960</i>	0.8	7.84E-05	DNA-directed RNA polymerase, beta subunit, <i>rpoB</i>
<i>SP1787</i>	1.5	6.31E-05	hypothetical protein	<i>SP1961</i>	0.7	2.45E-05	
<i>SP1860</i>	1.4	1.21E-04	choline transporter, <i>proWX</i>				
<i>SP1903</i>	1.5	1.01E-06	conserved hypothetical protein				
<i>SP1923</i>	1.4	1.29E-04	pneumolysin				
<i>SP1924</i>	1.4	2.47E-04	hypothetical protein				
			hypothetical protein				
<i>SP1925</i>	1.5	2.63E-04					
			hypothetical protein				
<i>SP1926</i>	1.7	2.41E-06					

<i>SP1972</i>	1.3	6.41E-05	membrane protein	<i>SP1968</i>	0.8	4.68E-05	phosphopantetheine adenylyltransferase, <i>coaD</i>
<i>SP2013</i>	1.5	6.47E-06	conserved hypothetical protein	<i>SP1970</i>	0.3	2.32E-11	aspartate--ammonia ligase, <i>asnA</i>
<i>SP2016</i>	1.9	3.96E-06	nicotinate-nucleotide pyrophosphorylase, <i>nadC</i>	<i>SP1994</i>	0.8	4.05E-05	aminotransferase, class I
<i>SP2020</i>	1.3	8.61E-04	transcriptional regulator, GntR family	<i>SP1997</i>	0.7	9.73E-06	Cof family protein
<i>SP2106</i>	3.2	6.99E-12	glycogen phosphorylase family protein	<i>SP2026</i>	0.6	1.71E-04	alcohol dehydrogenase, iron-containing
<i>SP2107</i>	3.4	1.76E-12	4-alpha-glucanotransferase	<i>SP2030</i>	0.7	7.97E-05	transketolase
<i>SP2151</i>	1.3	4.04E-04	carbamate kinase, <i>arcC</i>	<i>SP2040</i>	0.7	3.72E-05	putative jag protein
<i>SP2152</i>	1.6	1.70E-05	conserved hypothetical protein	<i>SP2041</i>	0.7	5.44E-05	SpoIIJ family protein
<i>SP2173</i>	1.6	8.93E-07	dltD protein	<i>SP2042</i>	0.8	4.32E-04	ribonuclease P protein component, <i>rnpA</i>
<i>SP2174</i>	1.6	3.60E-05	D-alanyl carrier protein, <i>dltC</i>	<i>SP2044</i>	0.7	8.25E-07	acetate kinase, <i>ackA</i>
<i>SP2175</i>	1.6	9.92E-08	dltB protein	<i>SP2054</i>	0.7	1.41E-04	conserved hypothetical protein
<i>SP2176</i>	1.8	1.62E-08	D-alanine-activating enzyme, <i>dltA</i>	<i>SP2055</i>	0.7	9.15E-06	alcohol dehydrogenase, zinc-containing
<i>SP2204</i>	1.3	8.76E-04	ribosomal protein L9, <i>rplI</i>	<i>SP2058</i>	0.6	7.13E-05	queuine tRNA-ribosyltransferase
<i>SP2205</i>	1.5	5.99E-07	DHH subfamily 1 protein	<i>SP2065</i>	0.8	1.98E-04	MATE efflux family protein
<i>SP2225</i>	1.2	9.61E-04	conserved hypothetical protein	<i>SP2069</i>	0.7	1.39E-05	glutamyl-tRNA synthetase, <i>gltX</i>
<i>SP2238</i>	1.9	6.58E-06	conserved hypothetical protein	<i>SP2078</i>	0.6	5.79E-08	arginyl-tRNA synthetase, <i>argS</i>
<i>SP2239</i>	3.0	6.94E-09	serine protease	<i>SP2081</i>	0.8	4.71E-05	conserved hypothetical protein
<i>SP2240</i>	3.5	1.35E-11	spspJ protein	<i>SP2108</i>	0.6	4.15E-07	maltose/maltodextrin ABC transporter, <i>malX</i>
				<i>SP2109</i>	0.6	7.41E-06	maltodextrin ABC transporter, permease protein, <i>malC</i>
				<i>SP2134</i>	0.6	2.53E-07	ribosomal protein L32, <i>rpmF</i>
				<i>SP2135</i>	0.6	3.62E-05	ribosomal protein L33, <i>rpmG-3</i>
				<i>SP2144</i>	0.7	8.16E-04	conserved hypothetical protein
				<i>SP2185</i>	0.6	2.51E-05	hypothetical protein
				<i>SP2186</i>	0.5	1.45E-06	glycerol kinase
				<i>SP2187</i>	0.8	7.59E-04	conserved domain protein
				<i>SP2188</i>	0.7	3.32E-07	chaperonin, 33 kDa, <i>hslO</i>
				<i>SP2189</i>	0.7	4.26E-05	putative TIM-barrel protein, NifR3 family
				<i>SP2214</i>	0.7	1.83E-05	translation elongation factor Ts
				<i>SP2215</i>	0.7	1.91E-05	ribosomal protein S2, <i>rpsB</i>
				<i>SP2216</i>	0.7	2.12E-04	secreted 45 kd protein, <i>usp45</i>
				<i>SP2218</i>	0.8	8.03E-05	rod shape-determining protein MreC
				<i>SP2230</i>	0.7	7.99E-05	ABC transporter, ATP-binding protein
				<i>SP2233</i>	0.3	1.52E-06	hypothetical protein

1 F. List of genes differentially expressed upon **30 min.** treatment with **LL-37**:

up-regulated genes				down-regulated genes			
Gene ID	Ratio	Bayes.p	NCBI annotation	Gene ID	Ratio	Bayes.p	NCBI annotation
<i>SP0057</i>	1.4	4.35E-04	beta-N-acetylhexosaminidase	<i>SP0024</i>	0.5	3.10E-06	Conserved hypothetical protein
<i>SP0071</i>	2.2	6.27E-05	zinc metalloprotease ZmpC	<i>SP0025</i>	0.6	4.78E-05	Hypothetical protein
<i>SP0088</i>	1.8	5.71E-07	hypothetical protein	<i>SP0026</i>	0.5	6.92E-05	Hypothetical protein
<i>SP0141</i>	1.7	1.28E-05	transcriptional regulator	<i>SP0034</i>	0.5	1.37E-06	membrane protein
<i>SP0143</i>	1.5	3.87E-05	conserved domain protein	<i>SP0117</i>	0.6	3.55E-04	pneumococcal surface protein A
<i>SP0144</i>	1.7	1.28E-05	hypothetical protein	<i>SP0239</i>	0.7	9.64E-04	conserved hypothetical protein
<i>SP0145</i>	1.5	2.10E-05	conserved hypothetical protein	<i>SP0281</i>	0.5	2.60E-06	aminopeptidase C, <i>pepC</i>
			ABC transporter, ATP-binding protein				PTS system, mannose-specific IID component
<i>SP0151</i>	1.4	2.06E-04	hypothetical protein	<i>SP0282</i>	0.3	4.30E-07	PTS system, mannose-specific IIC component, <i>manM</i>
<i>SP0157</i>	2.0	1.09E-07	riboflavin biosynthesis protein RibD	<i>SP0283</i>	0.3	1.52E-07	PTS system, mannose-specific IIAB components, <i>manL</i>
<i>SP0178</i>	1.5	5.20E-05	hypothetical protein	<i>SP0284</i>	0.2	2.54E-08	alcohol dehydrogenase, zinc-containing
<i>SP0184</i>	1.5	5.74E-06	magnesium transporter, CorA family	<i>SP0285</i>	0.6	3.24E-05	Cof family protein
<i>SP0185</i>	1.7	2.55E-05	conserved hypothetical protein	<i>SP0286</i>	0.7	3.40E-04	xanthine/uracil permease family protein
<i>SP0189</i>	1.7	1.95E-06	hypothetical protein	<i>SP0287</i>	0.6	4.48E-04	dihydropteroate synthase
<i>SP0190</i>	1.4	9.20E-04	hypothetical protein	<i>SP0289</i>	0.7	1.69E-04	dihydrofolate synthetase, <i>folC</i>
<i>SP0191</i>	1.4	3.22E-04	hypothetical protein	<i>SP0290</i>	0.7	2.68E-04	GTP cyclohydrolase I, <i>folE</i>
<i>SP0196</i>	1.5	5.50E-04	putative dihydrofolate synthetase	<i>SP0291</i>	0.7	5.74E-04	bifunctional folate synthesis protein, <i>sulD</i>
<i>SP0197</i>	1.5	6.42E-05	hypothetical protein	<i>SP0292</i>	0.7	2.05E-04	hypothetical protein
<i>SP0198</i>	1.3	9.14E-04	cardiolipin synthetase	<i>SP0293</i>	0.6	1.28E-05	oligopeptide ABC transporter
<i>SP0199</i>	1.5	2.01E-04	competence-induced protein Ccs4	<i>SP0366</i>	0.3	1.13E-09	oligopeptide-binding protein AliA
<i>SP0200</i>	1.6	3.40E-06	ribosomal protein L36	<i>SP0368</i>	0.6	9.29E-04	cell wall surface anchor family protein
<i>SP0233</i>	1.5	1.27E-04	ribosomal protein S13	<i>SP0411</i>	0.6	3.65E-06	seryl-tRNA synthetase, <i>serS</i>
<i>SP0234</i>	1.6	2.53E-06	ribosomal protein S11	<i>SP0413</i>	0.7	1.30E-04	aspartate kinase
<i>SP0235</i>	1.5	1.91E-05	DNA-directed RNA polymerase, alpha subunit, <i>rpoA</i>	<i>SP0435</i>	0.7	6.22E-04	translation elongation factor P
<i>SP0236</i>	1.5	3.63E-05	ribosomal protein L17	<i>SP0445</i>	0.6	1.35E-04	acetolactate synthase, large subunit, biosynthetic type, <i>ilvB</i>
<i>SP0237</i>	2.9	2.30E-07	undecaprenyl diphosphate synthase, <i>uupS</i>	<i>SP0446</i>	0.5	3.24E-08	acetolactate synthase, small subunit, <i>ilvN</i>
<i>SP0261</i>	1.7	4.50E-06		<i>SP0447</i>	0.5	8.68E-08	ketol-acid reductoisomerase, <i>ilvC</i>

SP0262	1.7	1.25E-06	phosphatidate cytidyltransferase	SP0448	0.5	2.03E-06	hypothetical protein
SP0263	1.4	5.45E-04	eep protein	SP0449	0.6	3.22E-04	hypothetical protein
SP0264	1.4	2.97E-04	prolyl-tRNA synthetase, <i>proS</i>	SP0450	0.7	5.78E-04	threonine dehydratase
			conserved hypothetical protein				amino acid ABC transporter, amino acid-binding protein/permease protein
SP0275	1.6	1.63E-05		SP0453	0.7	7.31E-04	
SP0276	1.5	3.23E-05	conserved hypothetical protein	SP0479	0.6	1.71E-05	potassium uptake protein, Trk family
SP0277	1.5	1.06E-04	hypothetical protein	SP0480	0.7	2.77E-04	potassium uptake protein, Trk family
SP0278	1.4	7.66E-04	aminopeptidase PepS	SP0516	0.6	3.04E-04	heat shock protein GrpE
			hypothetical protein; this gene contains a frame shift				DnaK protein
SP0331	1.9	3.81E-05		SP0517	0.5	6.00E-07	
SP0333	1.7	1.39E-05	putative transcriptional regulator	SP0518	0.6	9.03E-06	hypothetical protein
			capsular polysaccharide biosynthesis				dnaJ protein
SP0346	1.5	5.64E-05	protein Cps4A	SP0519	0.6	2.86E-05	
			capsular polysaccharide biosynthesis				conserved domain protein
SP0347	1.7	2.49E-05	protein Cps4B	SP0565	0.6	2.38E-05	
SP0369	2.2	2.47E-06	penicillin-binding protein 1A, <i>pbp1A</i>	SP0566	0.6	1.57E-04	acetyltransferase, GNAT family
SP0370	2.2	4.25E-06	recombination protein U, <i>recU</i>	SP0568	0.6	9.92E-06	valyl-tRNA synthetase, <i>valS</i>
			conserved hypothetical protein				PTS system, beta-glucosides-specific
SP0371	1.4	5.28E-04		SP0577	0.2	1.43E-11	IIABC
SP0372	1.5	1.56E-05	conserved hypothetical protein	SP0578	0.2	1.12E-11	6-phospho-beta-glucosidase, <i>bglA-2</i>
			conserved hypothetical protein				phenylalanyl-tRNA synthetase, alpha subunit, <i>pheS</i>
SP0385	1.6	2.34E-04		SP0579	0.5	1.22E-07	acetyltransferase, GNAT family
SP0386	1.7	1.06E-04	putative sensor histidine kinase	SP0580	0.5	1.91E-06	phenylalanyl-tRNA synthetase, beta subunit
			DNA-binding response regulator				fructose-bisphosphate aldolase
SP0387	1.5	3.08E-04		SP0581	0.5	9.45E-07	beta-lactam resistance factor, <i>fibA</i>
SP0402	1.5	1.30E-04	signal peptidase I	SP0605	0.6	1.76E-04	beta-lactam resistance factor, <i>fibB</i>
SP0403	1.5	2.85E-05	ribonuclease HIII, <i>rnhC</i>	SP0615	0.7	1.59E-04	
SP0404	1.6	1.74E-04	hypothetical protein	SP0616	0.7	1.35E-04	
SP0405	1.6	1.26E-04	conserved hypothetical protein	SP0730	0.5	3.64E-06	pyruvate oxidase, <i>spxB</i>
SP0408	2.1	2.38E-05	sodium:alanine symporter family protein	SP0731	0.6	2.07E-06	conserved domain protein
SP0409	1.5	3.01E-04	conserved hypothetical protein	SP0770	0.7	6.53E-04	ABC transporter, ATP-binding protein
			enoyl-CoA hydratase/isomerase family				peptidyl-prolyl cis-trans isomerase, cyclophilin-type
SP0415	1.9	1.27E-06	protein	SP0771	0.6	2.78E-05	
SP0416	1.6	2.11E-06	transcriptional regulator, MarR family	SP0775	0.6	5.04E-05	ribosomal protein S16, <i>rpsP</i>
			3-oxoacyl-(acyl-carrier-protein) synthase				lipoprotein
SP0417	1.8	6.64E-07	III, <i>fabH</i>	SP0845	0.4	4.40E-06	
SP0419	1.8	9.50E-07	enoyl-(acyl-carrier-protein) reductase,	SP0856	0.7	1.12E-04	branched-chain amino acid

<i>SP0420</i>	1.6	1.30E-05	<i>fabK</i> malonyl CoA-acyl carrier protein transacylase, <i>fabD</i>	<i>SP0857</i>	0.6	7.10E-04	aminotransferase, <i>ilvE</i> putative membrane protein
<i>SP0421</i>	1.6	3.38E-05	3-oxoacyl-[acyl-carrier protein] reductase, <i>fabG</i>	<i>SP0858</i>	0.6	2.95E-04	membrane protein
<i>SP0422</i>	1.4	1.12E-04	3-oxoacyl-(acyl-carrier-protein) synthase II, <i>fabF</i>	<i>SP0862</i>	0.7	5.33E-04	ribosomal protein S1, <i>rpsA</i>
<i>SP0423</i>	1.5	5.41E-05	acetyl-CoA carboxylase, biotin carboxyl carrier protein, <i>accB</i>	<i>SP0887</i>	0.6	1.29E-05	putative type I restriction-modification system, S subunit
<i>SP0424</i>	1.6	1.45E-05	(3R)-hydroxymyristoyl-(acyl-carrier- protein) dehydratase, <i>fabZ</i>	<i>SP1004</i>	0.6	1.24E-04	conserved hypothetical protein
<i>SP0425</i>	1.6	1.07E-05	acetyl-CoA carboxylase, biotin carboxylase, <i>accC</i>	<i>SP1008</i>	0.6	9.34E-06	peptidase t, <i>pepT</i>
<i>SP0426</i>	1.6	1.69E-05	acetyl-CoA carboxylase, carboxyl transferase, beta subunit, <i>accD</i>	<i>SP1013</i>	0.7	1.24E-04	aspartate-semialdehyde dehydrogenase
<i>SP0427</i>	2.1	8.26E-07	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit, <i>accA</i>	<i>SP1032</i>	0.6	3.24E-05	iron-compound ABC transporter, iron compound-binding protein
<i>SP0429</i>	1.7	1.36E-04	hypothetical protein	<i>SP1034</i>	0.7	4.24E-04	iron-compound ABC transporter, permease protein
<i>SP0430</i>	1.9	3.87E-05	hypothetical protein	<i>SP1035</i>	0.6	7.60E-04	iron-compound ABC transporter, ATP- binding protein
<i>SP0431</i>	1.6	2.66E-04	conserved domain protein	<i>SP1069</i>	0.6	1.68E-04	conserved hypothetical protein
<i>SP0484</i>	1.4	1.15E-04	cobalt transport protein	<i>SP1070</i>	0.6	4.65E-05	conserved hypothetical protein
<i>SP0489</i>	1.5	6.77E-05	PAP2 family protein	<i>SP1089</i>	0.6	2.59E-06	glutamine amidotransferase, class I
<i>SP0490</i>	1.5	2.02E-04	hypothetical protein	<i>SP1090</i>	0.6	1.47E-06	conserved hypothetical protein
<i>SP0491</i>	1.5	7.54E-04	hypothetical protein	<i>SP1114</i>	0.7	2.72E-04	ABC transporter, ATP-binding protein
<i>SP0492</i>	1.6	4.95E-05	conserved domain protein	<i>SP1119</i>	0.5	1.76E-05	glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent
<i>SP0496</i>	1.6	8.35E-05	Na/Pi cotransporter II-related protein transcriptional regulator, MerR family	<i>SP1128</i>	0.6	3.75E-04	enolase
<i>SP0501</i>	2.1	1.77E-05	hypothetical protein	<i>SP1167</i>	0.7	8.55E-04	dihydroorotase, multifunctional complex type, <i>pyrC</i>
<i>SP0502</i>	2.1	4.40E-06	glutamine synthetase, type I hypothetical protein	<i>SP1170</i>	0.5	6.74E-06	hypothetical protein
<i>SP0503</i>	1.7	9.69E-04	hypothetical protein	<i>SP1171</i>	0.5	1.20E-06	hydrolase, haloacid dehalogenase-like family
<i>SP0504</i>	2.0	2.41E-06	hypothetical protein	<i>SP1175</i>	0.5	2.17E-07	conserved domain protein
<i>SP0524</i>	1.8	1.33E-05	BlpT protein, fusion	<i>SP1182</i>	0.7	6.59E-06	lactose phosphotransferase system repressor, <i>lacR-2</i>
<i>SP0525</i>	1.8	2.25E-06	BlpS protein	<i>SP1185</i>	0.6	1.87E-05	PTS system, lactose-specific IIBC

<i>SP0526</i>	1.6	2.50E-06	response regulator BlpR	<i>SP1187</i>	0.5	2.70E-06	components, <i>lacE-2</i>
<i>SP0527</i>	1.8	2.47E-05	putative sensor histidine kinase BlpH	<i>SP1190</i>	0.7	4.65E-04	transcription antiterminator LacT
<i>SP0528</i>	1.8	2.75E-04	peptide pheromone BlpC	<i>SP1191</i>	0.7	7.67E-04	tagatose 1,6-diphosphate aldolase, <i>lacD</i>
<i>SP0529</i>	2.2	5.50E-09	BlpB ABC transporter	<i>SP1193</i>	0.7	6.94E-04	tagatose-6-phosphate kinase, <i>lacC</i>
<i>SP0530</i>	3.6	2.25E-09	BlpA ABC transporter	<i>SP1212</i>	0.6	1.02E-04	galactose-6-phosphate isomerase, LacA subunit, <i>lacA</i>
<i>SP0533</i>	1.5	1.50E-05	bacteriocin BlpK	<i>SP1294</i>	0.6	8.02E-04	tRNA pseudouridine synthase B, <i>truB</i>
<i>SP0545</i>	5.9	2.80E-11	immunity protein BlpY	<i>SP1295</i>	0.6	1.29E-05	crcB protein, <i>crcB-1</i>
<i>SP0546</i>	3.8	4.27E-10	BlpZ protein, fusion	<i>SP1298</i>	0.5	2.36E-08	crcB protein, <i>crcB-2</i>
<i>SP0547</i>	4.0	1.87E-08	conserved domain protein	<i>SP1383</i>	0.7	1.41E-04	DHH subfamily 1 protein
<i>SP0557</i>	1.8	5.88E-05	ribosome-binding factor A, <i>rbfA</i>	<i>SP1384</i>	0.7	6.11E-04	alanyl-tRNA synthetase, <i>alaS</i>
<i>SP0582</i>	2.2	6.33E-06	hypothetical protein	<i>SP1441</i>	0.7	9.41E-04	conserved hypothetical protein
<i>SP0589</i>	1.3	8.94E-04	serine acetyltransferase, <i>cysE</i>	<i>SP1445</i>	0.3	5.03E-10	This gene is interrupted by an RUP element
<i>SP0592</i>	1.5	1.80E-05	conserved hypothetical protein	<i>SP1462</i>	0.6	1.28E-05	GMP synthase, <i>guaA</i>
<i>SP0593</i>	1.6	7.21E-06	leucine-rich protein	<i>SP1463</i>	0.5	1.08E-06	conserved hypothetical protein
<i>SP0617</i>	1.5	1.40E-04	conserved domain protein	<i>SP1464</i>	0.6	1.40E-06	methylated-DNA--protein-cysteine S-methyltransferase
<i>SP0641</i>	1.5	7.95E-04	serine protease, subtilase family	<i>SP1469</i>	0.7	5.52E-04	acetyltransferase, GNAT family
<i>SP0655</i>	1.3	4.70E-04	transporter, monovalent cation:proton	<i>SP1474</i>	0.7	2.15E-04	NADH oxidase
<i>SP0656</i>	1.3	2.36E-04	antiporter-2 (CPA2) family	<i>SP1491</i>	0.7	3.12E-04	glycyl-tRNA synthetase, beta subunit, <i>glyS</i>
<i>SP0657</i>	1.4	4.65E-05	putative ribonuclease BN	<i>SP1500</i>	0.5	6.35E-06	putative glycerol uptake facilitator protein
<i>SP0742</i>	1.8	5.88E-05	cytochrome c-type biogenesis protein CcdA	<i>SP1501</i>	0.7	1.25E-05	amino acid ABC transporter, amino acid-binding protein
<i>SP0748</i>	1.4	3.92E-04	conserved hypothetical protein	<i>SP1502</i>	0.7	6.27E-05	amino acid ABC transporter, ATP-binding protein
<i>SP0762</i>	1.7	3.31E-06	conserved hypothetical protein	<i>SP1505</i>	0.7	5.63E-04	amino acid ABC transporter, permease protein
<i>SP0783</i>	2.3	8.25E-07	S-adenosylmethionine synthetase	<i>SP1508</i>	0.7	3.00E-04	membrane protein
<i>SP0785</i>	5.5	3.64E-12	conserved hypothetical protein	<i>SP1509</i>	0.6	7.45E-07	ATP synthase F1, beta subunit, <i>atpD</i>
<i>SP0786</i>	5.0	1.34E-07	ABC transporter, ATP-binding protein	<i>SP1510</i>	0.6	2.31E-06	ATP synthase F1, gamma subunit, <i>atpG</i>
<i>SP0787</i>	6.1	1.14E-09	conserved hypothetical protein	<i>SP1511</i>	0.6	1.74E-04	ATP synthase F1, alpha subunit, <i>atpA</i>
<i>SP0789</i>	1.6	1.94E-05	conserved hypothetical protein	<i>SP1512</i>	0.6	2.83E-05	ATP synthase F1, delta subunit, <i>atpH</i>
<i>SP0790</i>	1.5	1.25E-05	conserved hypothetical protein	<i>SP1513</i>	0.6	5.47E-06	ATP synthase F0, B subunit, <i>atpF</i>
<i>SP0798</i>	2.1	2.78E-04	DNA-binding response regulator CiaR	<i>SP1533</i>	0.7	1.99E-04	ATP synthase F0, A subunit, <i>atpB</i>
							conserved domain protein

<i>SP0800</i>	2.1	8.88E-06	sensor histidine kinase CiaH hydrolase, haloacid dehalogenase-like family	<i>SP1548</i>	0.6	6.34E-06	hypothetical protein polypeptide deformylase, <i>def-2</i>
<i>SP0805</i>	1.3	3.75E-04	conserved hypothetical protein, authentic point mutation	<i>SP1549</i>	0.6	1.32E-04	Lysozyme, <i>lytC</i>
<i>SP0827</i>	1.3	4.52E-04		<i>SP1573</i>	0.6	2.78E-05	
<i>SP0829</i>	1.5	6.63E-05	Phosphopentomutase, <i>deoB</i> ribosomal protein S20, <i>rpsT</i>	<i>SP1574</i>	0.7	4.02E-04	triosephosphate isomerase
<i>SP0838</i>	1.5	1.25E-04		<i>SP1580</i>	0.5	1.18E-07	sugar ABC transporter, ATP-binding protein, <i>msmK</i>
<i>SP0851</i>	1.4	7.64E-04	conserved hypothetical protein lactose phosphotransferase system	<i>SP1604</i>	0.7	3.23E-04	hypothetical protein ferredoxin
<i>SP0875</i>	2.2	6.03E-07	repressor	<i>SP1605</i>	0.6	2.95E-06	
<i>SP0876</i>	2.2	8.37E-07	putative 1-phosphofructokinase PTS system, fructose specific IIABC components	<i>SP1606</i>	0.6	1.47E-06	glycosyl transferase, family 2 UDP-glucose 4-epimerase, <i>galE-1</i>
<i>SP0877</i>	2.3	4.79E-07		<i>SP1607</i>	0.6	1.14E-05	
<i>SP0878</i>	1.6	8.50E-05	SpoE family protein	<i>SP1630</i>	0.7	2.24E-04	hypothetical protein
<i>SP0880</i>	1.6	1.90E-06	aminotransferase, class-V	<i>SP1631</i>	0.6	1.22E-05	threonyl-tRNA synthetase
<i>SP0881</i>	1.7	2.87E-06	thiazole biosynthesis protein ThiI	<i>SP1645</i>	0.7	6.61E-04	GTP pyrophosphokinase
<i>SP0895</i>	1.5	3.44E-05	DNA polymerase III, alpha subunit, <i>dnaE</i>	<i>SP1647</i>	0.5	4.45E-08	endopeptidase O, <i>pepO</i>
<i>SP0904</i>	1.3	5.93E-04	conserved hypothetical protein putative ABC transporter, permease protein	<i>SP1651</i>	0.5	6.17E-07	thiol peroxidase, <i>psaD</i> isoleucyl-tRNA synthetase, <i>ileS</i>
<i>SP0913</i>	1.8	3.15E-04	conserved hypothetical protein	<i>SP1659</i>	0.6	1.93E-05	
<i>SP0925</i>	1.4	9.27E-04		<i>SP1709</i>	0.5	1.27E-06	phosphoglycerate dehydrogenase- related protein
<i>SP0931</i>	1.6	3.87E-06	glutamate 5-kinase, <i>proB</i>	<i>SP1710</i>	0.7	9.46E-04	nitroreductase family protein
<i>SP0932</i>	1.3	4.32E-04	gamma-glutamyl phosphate reductase	<i>SP1711</i>	0.7	4.47E-04	primosomal protein DnaI
<i>SP0956</i>	1.7	3.30E-05	hypothetical protein	<i>SP1712</i>	0.7	4.64E-04	hypothetical protein
<i>SP0957</i>	2.2	2.63E-07	ABC transporter, ATP-binding protein hypothetical protein	<i>SP1717</i>	0.6	8.93E-05	ABC transporter, ATP-binding protein tryptophan synthase, alpha subunit, <i>trpA</i>
<i>SP0958</i>	2.2	2.47E-08		<i>SP1811</i>	0.4	6.87E-04	tryptophan synthase, beta subunit, <i>trpB</i>
<i>SP0974</i>	1.4	7.44E-04	putative preprotein translocase, SecG subunit	<i>SP1812</i>	0.5	6.23E-04	
<i>SP0975</i>	1.7	5.41E-07	exoribonuclease, VacB/Rnb family	<i>SP1813</i>	0.5	3.11E-05	N-(5'-phosphoribosyl)-anthranilate isomerase, <i>trpF</i>
<i>SP0976</i>	1.7	7.57E-06	SsrA-binding protein	<i>SP1815</i>	0.4	1.15E-06	anthranilate phosphoribosyltransferase, <i>trpD</i>
<i>SP0977</i>	1.7	2.67E-06	tellurite resistance protein TehB	<i>SP1816</i>	0.4	5.54E-06	anthranilate synthase component II, <i>trpG</i>
<i>SP1027</i>	2.7	2.18E-06	conserved hypothetical protein	<i>SP1817</i>	0.5	3.77E-04	anthranilate synthase component I, <i>trpE</i>

<i>SP1044</i>	1.9	2.31E-06	putative hydrolase	<i>SP1888</i>	0.7	2.08E-04	oligopeptide ABC transporter, ATP-binding protein AmiE
<i>SP1072</i>	1.3	4.27E-04	DNA primase, <i>dnaG</i>	<i>SP1889</i>	0.7	3.30E-04	oligopeptide ABC transporter, permease protein AmiD
<i>SP1075</i>	1.7	2.77E-05	glycosyl transferase CpoA	<i>SP1891</i>	0.6	3.50E-05	oligopeptide ABC transporter, oligopeptide-binding protein AmiA
<i>SP1076</i>	1.6	3.59E-05	glycosyl transferase, group 1	<i>SP1906</i>	0.6	1.82E-04	chaperonin, 60 kDa, <i>groEL</i>
<i>SP1077</i>	1.5	9.44E-06	conserved domain protein	<i>SP1907</i>	0.6	8.24E-05	chaperonin, 10 kDa, <i>groES</i>
<i>SP1093</i>	1.4	2.00E-04	hypothetical protein	<i>SP1968</i>	0.7	8.07E-04	phosphopantetheine adenylyltransferase, <i>coaD</i>
<i>SP1147</i>	1.5	4.36E-04	integrase/recombinase, phage integrase family, truncation	<i>SP1970</i>	0.4	2.49E-07	aspartate--ammonia ligase, <i>asnA</i>
<i>SP1148</i>	1.8	2.40E-07	IS630-Spn1, transposase Orf2	<i>SP1994</i>	0.6	2.13E-04	aminotransferase, class I
<i>SP1149</i>	1.8	2.48E-06	IS630-Spn1, transposase Orf1	<i>SP1997</i>	0.6	2.44E-04	Cof family protein
<i>SP1151</i>	1.6	4.87E-05	exonuclease RexB	<i>SP2026</i>	0.4	9.86E-08	alcohol dehydrogenase, iron-containing
<i>SP1152</i>	1.4	4.55E-04	exonuclease RexA	<i>SP2027</i>	0.6	1.29E-04	conserved hypothetical protein
<i>SP1153</i>	1.4	4.41E-04	hypothetical protein	<i>SP2028</i>	0.7	4.73E-04	phosphotyrosine protein phosphatase
<i>SP1162</i>	1.5	2.79E-04	putative acetoin dehydrogenase complex, E2 component, dihydrolipoamide acetyltransferase	<i>SP2030</i>	0.5	1.84E-04	transketolase
<i>SP1207</i>	1.4	7.39E-05	exodeoxyribonuclease VII, large subunit, xseA	<i>SP2044</i>	0.6	2.78E-04	acetate kinase
<i>SP1208</i>	1.4	1.92E-04	uridine kinase	<i>SP2058</i>	0.7	6.27E-04	queuine tRNA-ribosyltransferase
<i>SP1233</i>	1.5	9.59E-05	hypothetical protein	<i>SP2069</i>	0.6	7.74E-05	glutamyl-tRNA synthetase, <i>gltX</i>
<i>SP1234</i>	1.7	3.31E-05	transcriptional regulator, biotin repressor family	<i>SP2078</i>	0.6	1.22E-05	arginyl-tRNA synthetase, <i>argS</i>
<i>SP1240</i>	1.7	9.20E-06	conserved hypothetical protein	<i>SP2081</i>	0.7	8.95E-04	conserved hypothetical protein
<i>SP1241</i>	1.6	8.32E-05	amino acid ABC transporter, amino acid-binding protein/permease protein	<i>SP2109</i>	0.7	9.53E-04	maltodextrin ABC transporter, permease protein, <i>malC</i>
<i>SP1242</i>	1.8	5.22E-06	amino acid ABC transporter, ATP-binding protein	<i>SP2134</i>	0.7	7.36E-04	ribosomal protein L32, <i>rpmF</i>
<i>SP1275</i>	2.1	7.36E-06	carbamoyl-phosphate synthase, large subunit <i>carB</i>	<i>SP2188</i>	0.6	4.64E-05	chaperonin, 33 kDa, <i>hslO</i>
<i>SP1276</i>	1.9	1.06E-05	carbamoyl-phosphate synthase, small subunit, <i>carA</i>	<i>SP2189</i>	0.6	8.60E-05	putative TIM-barrel protein, NifR3 family
<i>SP1277</i>	1.7	1.76E-04	aspartate carbamoyltransferase, <i>pyrB</i>	<i>SP2230</i>	0.6	1.08E-04	ABC transporter, ATP-binding protein
<i>SP1315</i>	1.5	4.95E-05	v-type sodium ATP synthase, subunit D, <i>ntpD</i>	<i>SP2231</i>	0.5	2.04E-06	putative ABC transporter, permease protein

<i>SP1380</i>	1.6	2.61E-05	hypothetical protein	<i>SP2232</i>	0.4	6.15E-05	nserved hypothetical protein, authentic
<i>SP1381</i>	1.6	7.21E-05	ABC transporter, ATP-binding protein	<i>SP2233</i>	0.3	1.47E-06	frame shift
<i>SP1388</i>	1.3	6.66E-04	spermidine/putrescine ABC transporter, permease protein	<i>SP2234</i>	0.5	3.09E-05	hypothetical protein
<i>SP1390</i>	1.3	4.62E-04	UDP-N-acetylenolpyruvoylglucosamine reductase, <i>murB</i>	<i>SP2235</i>	0.7	7.63E-04	transcriptional regulator, TetR family
<i>SP1392</i>	1.3	8.55E-04	alpha-acetolactate decarboxylase, <i>aldB</i>				response regulator ComE
<i>SP1405</i>	1.5	1.24E-05	conserved hypothetical protein				
<i>SP1426</i>	1.4	3.94E-04	ABC transporter, ATP-binding protein				
<i>SP1479</i>	1.4	9.25E-04	peptidoglycan N-acetylglucosamine deacetylase A, <i>pgdA</i>				
<i>SP1521</i>	1.5	7.17E-04	UDP-N-acetylmuramate--alanine ligase, <i>murC</i>				
<i>SP1522</i>	1.4	4.23E-04	conserved domain protein				
<i>SP1523</i>	1.4	7.00E-04	Snf2 family protein				
<i>SP1546</i>	1.7	1.71E-05	conserved domain protein				
<i>SP1560</i>	1.5	1.62E-05	conserved hypothetical protein				
<i>SP1561</i>	1.6	6.49E-06	conserved hypothetical protein				
<i>SP1562</i>	1.6	4.26E-06	hypothetical protein				
<i>SP1600</i>	1.7	8.74E-06	putative membrane protein				
<i>SP1602</i>	1.4	4.80E-04	phnA protein				
<i>SP1623</i>	1.7	4.43E-06	cation-transporting ATPase, E1-E2 family				
<i>SP1625</i>	1.4	9.69E-04	putative cadmium resistance transporter				
<i>SP1636</i>	1.4	2.71E-04	Rrf2 family protein				
<i>SP1640</i>	1.6	2.09E-06	hypothetical protein				
<i>SP1641</i>	1.6	2.22E-05	Conserved hypothetical protein				
<i>SP1668</i>	1.6	4.06E-05	hypothetical protein				
<i>SP1669</i>	1.3	3.04E-04	MutT/nudix family protein				
<i>SP1670</i>	1.3	8.29E-04	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase, <i>murF</i>				
<i>SP1671</i>	1.4	3.06E-04	D-alanine--D-alanine ligase, <i>ddlA</i>				
<i>SP1674</i>	1.6	2.42E-06	putative phosphosugar-binding transcriptional regulator				
<i>SP1695</i>	2.3	6.74E-05	putative acetyl xylan esterase				
<i>SP1696</i>	2.5	3.28E-05	hypothetical protein				

<i>SP1714</i>	9.1	9.49E-14	transcriptional regulator, GntR family				
<i>SP1715</i>	13.0	2.33E-15	ABC transporter, ATP-binding protein				
<i>SP1720</i>	1.3	9.91E-04	conserved hypothetical protein				
<i>SP1752</i>	1.4	3.56E-04	putative mechanosensitive ion channel				
<i>SP1774</i>	1.6	1.44E-06	putative transcriptional regulator				
<i>SP1776</i>	1.5	3.55E-05	thioredoxin				
<i>SP1786</i>	1.9	7.55E-07	conserved hypothetical protein				
<i>SP1787</i>	1.8	3.07E-07	hypothetical protein				
<i>SP1860</i>	1.8	2.85E-07	choline transporter, <i>proWX</i>				
<i>SP1861</i>	1.7	1.96E-06	choline transporter, <i>proV</i>				
<i>SP1862</i>	1.5	1.02E-04	hypothetical protein				
<i>SP1863</i>	1.5	1.18E-05	transcriptional regulator, MarR family				
<i>SP1903</i>	1.6	3.27E-05	conserved hypothetical protein				
<i>SP1926</i>	1.5	3.74E-05	hypothetical protein				
<i>SP1938</i>	1.6	4.12E-04	hypothetical protein				
<i>SP1939</i>	1.5	5.01E-05	MATE efflux family protein DinF				
<i>SP1972</i>	1.4	5.69E-04	membrane protein				
<i>SP2007</i>	1.5	5.76E-04	transcription antitermination protein NusG				
<i>SP2009</i>	1.5	6.82E-05	ribosomal protein L33, <i>rpmG-2</i>				
<i>SP2013</i>	1.9	4.11E-08	conserved hypothetical protein				
<i>SP2016</i>	2.0	3.92E-07	nicotinate-nucleotide pyrophosphorylase, <i>nadC</i>				
<i>SP2062</i>	1.5	4.84E-04	transcriptional regulator, MarR family				
<i>SP2106</i>	2.6	4.50E-06	glycogen phosphorylase family protein				
<i>SP2107</i>	2.9	5.56E-06	4-alpha-glucanotransferase, <i>malQ</i>				
<i>SP2148</i>	1.5	4.07E-06	arginine deiminase, <i>arcA</i>				
<i>SP2150</i>	1.4	9.24E-05	ornithine carbamoyltransferase, <i>argF</i>				
<i>SP2151</i>	1.6	2.33E-06	carbamate kinase, <i>arcC</i>				
<i>SP2152</i>	1.9	2.88E-07	conserved hypothetical protein				
<i>SP2153</i>	1.5	1.51E-04	peptidase, M20/M25/M40 family				
<i>SP2202</i>	1.6	7.03E-05	conserved hypothetical protein				
<i>SP2205</i>	1.5	2.67E-05	DHH subfamily 1 protein				
<i>SP2226</i>	1.3	8.27E-04	conserved hypothetical protein				
<i>SP2239</i>	2.3	8.74E-05	serine protease				
<i>SP2240</i>	2.2	7.51E-04	spspoJ protein				

1
2
3
4
5

Table S.2. List of genes commonly up- and down-regulated upon **15 and 30** min.

A : treatment with each AMP:

Bacitracin	Nisin	LL-37					
<i>SP0430</i>	<i>SP0415</i>	<i>SP0071</i>	<i>SP0447</i>	<i>SP0787</i>	<i>SP1193</i>	<i>SP1695</i>	<i>SP2188</i>
<i>SP0785</i>	<i>SP0501</i>	<i>SP0024</i>	<i>SP0448</i>	<i>SP0789</i>	<i>SP1212</i>	<i>SP1696</i>	<i>SP2189</i>
<i>SP0786</i>	<i>SP0502</i>	<i>SP0025</i>	<i>SP0450</i>	<i>SP0790</i>	<i>SP1241</i>	<i>SP1709</i>	<i>SP2205</i>
<i>SP0787</i>	<i>SP0876</i>	<i>SP0026</i>	<i>SP0479</i>	<i>SP0798</i>	<i>SP1242</i>	<i>SP1710</i>	<i>SP2230</i>
<i>SP0910</i>	<i>SP0875</i>	<i>SP0034</i>	<i>SP0496</i>	<i>SP0800</i>	<i>SP1380</i>	<i>SP1711</i>	<i>SP2233</i>
<i>SP0912</i>	<i>SP0912</i>	<i>SP0088</i>	<i>SP0501</i>	<i>SP0805</i>	<i>SP1381</i>	<i>SP1712</i>	<i>SP2239</i>
<i>SP0913</i>	<i>SP0913</i>	<i>SP0117</i>	<i>SP0502</i>	<i>SP0829</i>	<i>SP1383</i>	<i>SP1714</i>	<i>SP2240</i>
<i>SP1480</i>	<i>SP1241</i>	<i>SP0157</i>	<i>SP0503</i>	<i>SP0845</i>	<i>SP1405</i>	<i>SP1715</i>	
<i>SP2086</i>	<i>SP1242</i>	<i>SP0185</i>	<i>SP0504</i>	<i>SP0851</i>	<i>SP1445</i>	<i>SP1717</i>	
	<i>SP1588</i>	<i>SP0197</i>	<i>SP0516</i>	<i>SP0875</i>	<i>SP1462</i>	<i>SP1752</i>	
	<i>SP1648</i>	<i>SP0200</i>	<i>SP0517</i>	<i>SP0876</i>	<i>SP1463</i>	<i>SP1774</i>	
	<i>SP1649</i>	<i>SP0234</i>	<i>SP0518</i>	<i>SP0877</i>	<i>SP1464</i>	<i>SP1776</i>	
	<i>SP1871</i>	<i>SP0237</i>	<i>SP0519</i>	<i>SP0878</i>	<i>SP1469</i>	<i>SP1786</i>	
	<i>SP1872</i>	<i>SP0239</i>	<i>SP0524</i>	<i>SP0887</i>	<i>SP1479</i>	<i>SP1787</i>	
		<i>SP0261</i>	<i>SP0525</i>	<i>SP0895</i>	<i>SP1491</i>	<i>SP1811</i>	
		<i>SP0281</i>	<i>SP0526</i>	<i>SP0904</i>	<i>SP1500</i>	<i>SP1812</i>	
		<i>SP0282</i>	<i>SP0527</i>	<i>SP0913</i>	<i>SP1508</i>	<i>SP1813</i>	
		<i>SP0283</i>	<i>SP0529</i>	<i>SP0925</i>	<i>SP1509</i>	<i>SP1815</i>	
		<i>SP0284</i>	<i>SP0530</i>	<i>SP0956</i>	<i>SP1510</i>	<i>SP1816</i>	
		<i>SP0285</i>	<i>SP0533</i>	<i>SP0957</i>	<i>SP1511</i>	<i>SP1817</i>	
		<i>SP0287</i>	<i>SP0545</i>	<i>SP0958</i>	<i>SP1512</i>	<i>SP1860</i>	
		<i>SP0289</i>	<i>SP0546</i>	<i>SP0974</i>	<i>SP1513</i>	<i>SP1888</i>	

<i>SP0290</i>	<i>SP0547</i>	<i>SP0975</i>	<i>SP1533</i>	<i>SP1891</i>
<i>SP0291</i>	<i>SP0557</i>	<i>SP0976</i>	<i>SP1546</i>	<i>SP1903</i>
<i>SP0292</i>	<i>SP0565</i>	<i>SP0977</i>	<i>SP1548</i>	<i>SP1906</i>
<i>SP0293</i>	<i>SP0566</i>	<i>SP1013</i>	<i>SP1549</i>	<i>SP1907</i>
<i>SP0366</i>	<i>SP0568</i>	<i>SP1027</i>	<i>SP1560</i>	<i>SP1926</i>
<i>SP0369</i>	<i>SP0577</i>	<i>SP1032</i>	<i>SP1561</i>	<i>SP1968</i>
<i>SP0370</i>	<i>SP0578</i>	<i>SP1034</i>	<i>SP1562</i>	<i>SP1970</i>
<i>SP0372</i>	<i>SP0579</i>	<i>SP1035</i>	<i>SP1574</i>	<i>SP1972</i>
<i>SP0385</i>	<i>SP0581</i>	<i>SP1069</i>	<i>SP1580</i>	<i>SP1997</i>
<i>SP0386</i>	<i>SP0582</i>	<i>SP1070</i>	<i>SP1605</i>	<i>SP2013</i>
<i>SP0402</i>	<i>SP0589</i>	<i>SP1075</i>	<i>SP1607</i>	<i>SP2016</i>
<i>SP0403</i>	<i>SP0592</i>	<i>SP1076</i>	<i>SP1623</i>	<i>SP2026</i>
<i>SP0404</i>	<i>SP0593</i>	<i>SP1077</i>	<i>SP1625</i>	<i>SP2030</i>
<i>SP0405</i>	<i>SP0617</i>	<i>SP1093</i>	<i>SP1636</i>	<i>SP2044</i>
<i>SP0408</i>	<i>SP0730</i>	<i>SP1148</i>	<i>SP1640</i>	<i>SP2058</i>
<i>SP0413</i>	<i>SP0731</i>	<i>SP1149</i>	<i>SP1641</i>	<i>SP2069</i>
<i>SP0415</i>	<i>SP0742</i>	<i>SP1151</i>	<i>SP1645</i>	<i>SP2078</i>
<i>SP0416</i>	<i>SP0748</i>	<i>SP1162</i>	<i>SP1647</i>	<i>SP2081</i>
<i>SP0417</i>	<i>SP0762</i>	<i>SP1171</i>	<i>SP1659</i>	<i>SP2106</i>
<i>SP0419</i>	<i>SP0770</i>	<i>SP1175</i>	<i>SP1668</i>	<i>SP2107</i>
<i>SP0424</i>	<i>SP0775</i>	<i>SP1185</i>	<i>SP1669</i>	<i>SP2109</i>
<i>SP0427</i>	<i>SP0783</i>	<i>SP1187</i>	<i>SP1670</i>	<i>SP2134</i>
<i>SP0445</i>	<i>SP0785</i>	<i>SP1190</i>	<i>SP1671</i>	<i>SP2151</i>
<i>SP0446</i>	<i>SP0786</i>	<i>SP1191</i>	<i>SP1674</i>	<i>SP2152</i>

1

2 B List of genes commonly regulated upon **15 and 30** min. treatment with:

3

Nisin and LL-37	Bacitracin and LL-37	Bacitracin and nisin	Bacitracin, nisin and LL-37
<i>SP0415</i>	<i>SP0785</i>	<i>SP0912</i>	<i>SP0913</i>

<i>SP0875</i>	<i>SP0786</i>		
<i>SP0876</i>	<i>SP0787</i>		
<i>SP0501</i>			
<i>SP0502</i>			
<i>SP1241</i>			
<i>SP1242</i>			

1

2

3 **Table S.3. List of genes whose expression changed significantly in more than 1 stress and depicted in FIG. 1.**

4 **A.** List of genes commonly **down-regulated** after 15 or 30 min. upon treatment with:

nisin and LL-37	bacitracin and LL-37
<i>SP0285</i>	<i>SP0117</i>
<i>SP0366</i>	<i>SP0281</i>
<i>SP0578</i>	<i>SP0285</i>
<i>SP0577</i>	<i>SP0366</i>
<i>SP0731</i>	<i>SP0435</i>
<i>SP0922</i>	<i>SP0453</i>
<i>SP1187</i>	<i>SP0516</i>
<i>SP1507</i>	<i>SP0565</i>
<i>SP1970</i>	<i>SP0566</i>
<i>SP2055</i>	<i>SP0568</i>
<i>SP2108</i>	<i>SP0577</i>
	<i>SP0579</i>
	<i>SP0580</i>
	<i>SP0581</i>
	<i>SP0731</i>
	<i>SP0770</i>
	<i>SP0775</i>
	<i>SP1175</i>

	<i>SP1383</i>
	<i>SP1384</i>
	<i>SP1441</i>
	<i>SP1474</i>
	<i>SP1533</i>
	<i>SP1630</i>
	<i>SP1631</i>
	<i>SP1651</i>
	<i>SP1659</i>
	<i>SP1906</i>
	<i>SP2026</i>
	<i>SP2134</i>
	<i>SP2188</i>
	<i>SP2189</i>

1

2 **B.** List of genes commonly **up-regulated** upon 15 min. treatment with:

bacitracin and LL-37	nisin and LL-37	nisin and bacitracin	bacitracin, nisin and LL-37
<i>SP0385</i>	<i>SP0185</i>	<i>SP0912</i>	<i>SP0913</i>
<i>SP0386</i>	<i>SP0415</i>		
<i>SP0419</i>	<i>SP0416</i>		
<i>SP0424</i>	<i>SP0851</i>		
<i>SP0427</i>	<i>SP0875</i>		
<i>SP0785</i>	<i>SP0876</i>		
<i>SP0786</i>	<i>SP2173</i>		
<i>SP0787</i>			
<i>SP0861</i>			
<i>SP0910</i>			
<i>SP1714</i>			
<i>SP1715</i>			
<i>SP1925</i>			

<i>SP1926</i>			
---------------	--	--	--

1

2 **C. List of genes commonly *up-regulated* upon 30 min. treatment with:**

bacitracin and LL-37	nisin and LL-37	bacitracin and nisin	bacitracin, nisin and LL-37
<i>SP0088</i>	<i>SP0415</i>	<i>SP0912</i>	<i>SP0875</i>
<i>SP0157</i>	<i>SP0419</i>	<i>SP0913</i>	<i>SP0876</i>
<i>SP0189</i>	<i>SP0422</i>		<i>SP0913</i>
<i>SP0275</i>			<i>SP2062</i>
<i>SP0276</i>			
<i>SP0278</i>			
<i>SP0369</i>			
<i>SP0370</i>			
<i>SP0371</i>			
<i>SP0408</i>			
<i>SP0582</i>			
<i>SP0641</i>			
<i>SP0785</i>			
<i>SP0786</i>			
<i>SP0787</i>			
<i>SP0790</i>			
<i>SP0800</i>			
<i>SP0877</i>			
<i>SP1148</i>			
<i>SP1674</i>			
<i>SP1774</i>			
<i>SP1786</i>			
<i>SP1787</i>			

3

1

2 **Table S.4. List of genes differentially regulated by more than one AMP at either time point**

3

4

A. List of genes induced upon **15 or 30** min. treatment with:

Bacitracin, nisin and LL-37	Bacitracin and LL-37	Bacitracin and nisin	Nisin and LL-37
<i>SP0419</i>	<i>SP0088</i>	<i>SP0912</i>	<i>SP0185</i>
<i>SP0422</i>	<i>SP0157</i>	<i>SP1343</i>	<i>SP0415</i>
<i>SP0641</i>	<i>SP0189</i>	<i>SP1588</i>	<i>SP0416</i>
<i>SP0875</i>	<i>SP0275</i>	<i>SP2063</i>	<i>SP0851</i>
<i>SP0876</i>	<i>SP0276</i>		<i>SP2173</i>
<i>SP0913</i>	<i>SP0278</i>		
<i>SP2062</i>	<i>SP0369</i>		
	<i>SP0370</i>		
	<i>SP0371</i>		
	<i>SP0385</i>		
	<i>SP0386</i>		
	<i>SP0387</i>		
	<i>SP0408</i>		
	<i>SP0420</i>		
	<i>SP0421</i>		
	<i>SP0424</i>		
	<i>SP0426</i>		
	<i>SP0427</i>		
	<i>SP0430</i>		
	<i>SP0582</i>		
	<i>SP0785</i>		
	<i>SP0786</i>		
	<i>SP0787</i>		

<i>SP0790</i>		
<i>SP0800</i>		
<i>SP0861</i>		
<i>SP0877</i>		
<i>SP0910</i>		
<i>SP1148</i>		
<i>SP1674</i>		
<i>SP1714</i>		
<i>SP1715</i>		
<i>SP1774</i>		
<i>SP1786</i>		
<i>SP1787</i>		
<i>SP1925</i>		
<i>SP1926</i>		

1

2 B. List of genes commonly down-regulated upon **15 or 30** min. treatment with:

Bacitracin, nisin and LL-37	Nisin and LL-37	Bacitracin and LL-37
<i>SP0285</i>	<i>SP0578</i>	<i>SP0117</i>
<i>SP0366</i>	<i>SP1187</i>	<i>SP0281</i>
<i>SP0731</i>	<i>SP1295</i>	<i>SP0435</i>
<i>SP0922</i>	<i>SP1507</i>	<i>SP0453</i>
<i>SP2055</i>	<i>SP1970</i>	<i>SP0459</i>
	<i>SP2108</i>	<i>SP0516</i>
		<i>SP0565</i>
		<i>SP0566</i>
		<i>SP0568</i>
		<i>SP0577</i>
		<i>SP0579</i>
		<i>SP0580</i>
		<i>SP0581</i>
		<i>SP0736</i>

	<i>SP0770</i>
	<i>SP0775</i>
	<i>SP0920</i>
	<i>SP1175</i>
	<i>SP1383</i>
	<i>SP1384</i>
	<i>SP1441</i>
	<i>SP1468</i>
	<i>SP1474</i>
	<i>SP1533</i>
	<i>SP1576</i>
	<i>SP1630</i>
	<i>SP1631</i>
	<i>SP1651</i>
	<i>SP1659</i>
	<i>SP1906</i>
	<i>SP2026</i>
	<i>SP2134</i>
	<i>SP2188</i>
	<i>SP2189</i>

1	
2	
3	
4	
5	
6	
7	